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Property on 3rd April 2002, from French into English;

THAT the attached English translation is a true and correct translation of
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to the best of my knowledge and belief; and

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JOHN CHARLES McGILLEY

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A

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PATENT OF INVENTION

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Drawn up in Paris 11th March 2005

For the Director General of the
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The Head of the Patent
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[signed]
Martine PLANCHE

1st filing
B

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PATENT OF INVENTION

Intellectual Property Code – Book VI
REQUEST FOR GRANT

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1 NATURE OF APPLICATION			
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2 TITLE OF INVENTION			
		MEANS FOR IDENTIFYING NEISSERIA MENINGITIDIS-SPECIFIC GENES	
3 DECLARATION OF PRIORITY OR REQUEST FOR BENEFIT FROM THE FILING DATE OF A PREVIOUS FRENCH APPLICATION		Country or organization	Date No.
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6 ATTACHED DOCUMENTS AND FILES		Electronic file	Pages Details

Description	desc.pdf.	8		
Claims	√	2	10	
Drawings		163	24 fig., 3 ex.	
Abstract	√	1		
Sequence listing, PDF				
Search report				
Cheque		1 doc.	0002137	
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Method of payment	Remittance of cheque			
Cheque No.	0002137			
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062 Filing	EURO	35.00	1.00	35.00
063 Search report (S.R.)	EURO	320.00	1.00	320.00
064 Declaration of a right to priority	EURO	15.00	1.00	15.00
Total to pay	EURO			370.00
10. SIGNATURE OF APPLICANT OR REPRESENTATIVE				
Signed by	Chantal PEAUCELLE			
	(signed)			

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Means for identifying *Neisseria meningitidis*-specific genes.

The invention relates to means for identifying genes specific to *Neisseria meningitidis* (Nm in abstract). It also relates to these genes and their biological applications.

Nm is a strictly human bacteria which does not survive in the external environment. It's only known reservoir is the nasopharynx of humans. In certain circumstances which are still little understood, this bacteria will leave the nasopharynx, infiltrate the blood in circulation and cause septicaemia and/or meningitides. The existence of a meningitis suggests that the bacteria crosses the blood-brain barrier, one of the most difficult barriers to cross in the organism. *Neisseria meningitidis* is a bacteria having extracellular multiplication, in other words its dissemination *in vivo* is accompanied by a multiplication in the interstitial area. Very few bacteria having extracellular multiplication are capable of crossing the blood-brain barrier after the neonatal period, they are essentially *Streptococcus pneumoniae*, *Haemophilus influenzae* and *Neisseria meningitidis*. This property thus suggests specific attributes which allow these microorganisms to cross this barrier.

Neisseria meningitidis presents two specificities for a bacteria having extracellular multiplication:

(i) It is responsible for substantial bacteremia with a high number of bacteria in the blood. Thus, the comparison, in an animal model using the new-born rat, of the level of bacteremia induced by the injection of the same number of bacteria belonging to two different species (*Neisseria meningitidis* and *Klebsiella pneumoniae*) shows that *N. meningitidis* induces a bacteremia which can be 50-100 times greater than that induced by *K. pneumoniae*. This underlines the perfect adaptation of *N. meningitidis* to growth in the extra-cellular area. Certain bacterial attributes have already been identified as participating in this extracellular growth. These are essentially the polysaccharidic capsule, the lipooligosaccharide and the iron capture systems. The two first attributes allow resistance to the complement and to

phagocytosis by the granulocytes and the third attribute allows the bacteria to obtain the iron essential for its growth.

(ii) The second particularity of *N. meningitidis* is related to its ability to cross the blood-brain barrier. This property results from an interaction with the cerebral endothelial cells. Until now the only bacterial attribute identified as being involved in the interaction of *N. meningitidis* at the cerebral endothelium level are the type IV pili. A molecule which is one of these pili called PilC, involved in this interaction, is the adhesin of the pili.

The inventors work has concerned the search for means allowing identification of the genes of Nm which are capable of growing specifically in serum and of crossing the blood-brain barrier.

The application to Nm of the technique described by Pelicic et al, 2000 for building a bank of mutants allowed mutagenization of more than 70% of the mutagenizable and thus non essential genes.

This tool has proved to be particularly valuable for detecting in an exhaustive fashion all of the mutants for a given phenotype, for example those which are important for growth in the serum, and for identifying adhesins which are important for interaction with the endothelial cells and thus the crossing of the blood-brain barrier and this is without necessarily testing the mutants individually for this phenotype.

Therefore the invention relates to the use of such a bank for detecting genes of Nm expressing a particular phenotype.

It also relates to the genes involved in such a phenotype.

The invention also relates to the exploitation of the thus-identified genes as Nm anti-pathogenicity targets.

It also relates to the use of the genes coding for adhesins to allow therapeutic ingredients to pass through the blood-brain barrier.

The invention moreover relates to the essential genes of *N. meningitidis*, and their homologues in other bacterial species and their use as targets for developing antibiotics.

According to the invention, genes of pathogenic bacteria, in particular of Nm, are detected, expressing a desired phenotype, according to a method characterized in that :

- a bank of mutants generated from a given bacterial strain is used so that at least 70 % of the non-essential genes, and in particular 80 %, or even more than 90 %, are mutagenized by inserting a transposon in a reading frame,

5 - the mutants are then brought into contact, either individually, or in pools, with an environment, such as a medium, an animal or cells, capable of interacting with the mutant bacteria expressing the desired phenotype,

- when pools are used, the bacteria which have not reacted with the desired phenotype are recovered,

10 - the mutated genes of these bacteria are identified and their involvement in said phenotype is verified.

The bank of mutants is advantageously generated according to the method described by Pelicic et al. above.

15 The contact stage is carried out by passing on serum or an animal model *in vivo* or cells which are able to react with the bacteria expressing the desired phenotype and, when pools of mutants are used, the bacteria which have not reacted with the desired phenotype are recovered.

20 In order to identify the mutated genes of these bacteria and to verify their involvement in said phenotype, the mutants are organized into pools. For each mutant, the insertion sites are amplified using appropriate oligonucleotides. The amplification products are placed on a membrane made for example of nylon. The pools of mutants are placed under the conditions for which mutants are sought. Total DNA is prepared using bacteria obtained from each output pool and an amplification is carried out using
25 oligonucleotides which served to amplify the insertion sites in the mutants of the pool. The amplification product then serves to hybridize the membranes which correspond to each pool. The mutants for which no amplification is detected are mutants for the phenotype considered. It will be observed that this technique allows the mutants in question to be retained, allowing each
30 mutation to be retransformed in order to confirm the phenotype.

The invention also relates to the genes which give a bacteria the ability to grow or to react with a given environment such as serum, an animal model *in vivo*, cells.

These genes are characterized in that they can be obtained by the method defined above.

In particular the invention relates to the genes involved in the growth of bacteria in serum, chosen from the genes of Figure 3, identified with respect to the number of the pool of mutants of Figure 2.

Quite particularly the invention relates to the genes Nm 83 dxr, Nm 229, Nm 356, Nm 848 galU, and the genes of serogroup B, Nm 1771 and NmB 65 as new products.

The invention also relates to the application of the genes selected in relation to the growth phenotype in serum, as anti-pathogenicity targets, which consists of inhibiting the growth of Nm *in vivo* in serum.

Other genes of great interest according to the invention are characterized in that they are involved in the interaction with endothelial cells.

Therefore the invention also relates to the application of these genes to allow the opening of the blood-brain barrier to therapeutic ingredients, such as medicaments for Parkinson's Disease, Alzheimer's disease, antimitotics, medicaments for multiple sclerosis, antivirals, antimycotics and antibiotics.

Moreover the invention relates to the essential genes of Nm for which no mutant is present in the bank and the application of these genes as targets for developing antibiotics.

Other characteristics and advantages of the invention are given in the examples which follow and with reference to Figures 1 to 24 which represent:

- Figure 1, the list of genes presenting in the 2 sequenced strains of Nm more than 65% similarity on a proteinic base,
- Figure 2A, the list of genes for which there exists a mutant in the bank and Figure 2B the list of mutants classified into 96 pools of 48 mutants,
- Figure 3, the list of the mutants altered in growth in the serum, and
- Figures 4 to 24, the growth curves of the mutants of Figure 3 in the complemented serum and the decomplexed serum.

• Construction of a bank of mutants of Nm 8013

1. A bank of mutants is built from the *N. meningitidis* 8013 strain of serogroup C, operating according to the technique described by Pelicic et al,

Journal of Bacteriology, 2000, 182: 5391-5398. A sequenced bank of 4547 mutants is obtained.

Statistically 80% of the insertions are in open reading frames since it concerns the % of coding regions in the genome of the 2 sequenced strains, namely Z2491, strain of serogroup A sequenced by the Sanger Center, and MC58, strain of serogroup B sequenced by TIGR. Therefore there are approximately 3600 mutants in open reading frames and in most cases, several insertions per gene. Taking into account the size of the genome, the mutagenesis thus concerns 93% of the mutagenizable genes.

The statistic formula allowing calculation of the probability (P) that a gene is mutated is the following:

$$P=1-e^{-n/P}$$

n: number of mutants in the bank

p: number of mutagenizable (non-essential) genes

The second number can only be estimated. But according to studies of bacteria better characterized than *Neisseria meningitidis*, it is reasonable to estimate that 350 genes are essential to the survival of the bacteria. Consequently, there would be 1750 non-essential genes in the meningococcus, 92.6 % (1619) of which should be mutated in the bank.

2. All of the insertions of this bank are sequenced according to the technique used for the sequencing of insertions, already described and published (Prod'hom *et al.* 1998. *FEMS Microbiol Lett.* 1858: 75-81). This technique uses a specific primer for the known sequence, in this case the transposon, and a second specific primer of a synthetic linker ligated to the reduced genomic DNA. The use of AmpliTaq Gold polymerase Perkin-Elmer is important for minimizing a non-specific hybridization of the primers.

• Determination of the essential genes.

An essential gene can be present only in a single strain. Any gene present in the two strains, the genome of which has been sequenced and for which a mutant does not exist in the bank of the invention is thus considered to be essential.

The genes present in the two strains are given in Figure 1. The nomenclature used is that of the strain Z2491 (sequenced by Sanger). The list given in Figure 1 was obtained by performing a TblastN of each reading frame of Z2491 in MC58, then keeping all the frames of Z2491 which had a
5 homology percentage greater than 65 %.

The list of the genes for which a mutant is present in the bank is represented in Figure 2A. The list of differential genes, i.e. those present in Figure 1 and not in Figure 2A, is high in essential genes. This list of differential genes includes genes which are homologous in other Gram-
10 negative pathogenic bacteria, such as enterobacteria, Pseudomonas, Acinetobacter, or even certain Gram-positive bacteria. These genes constitute targets for developing broad spectrum antibiotics against these Gram-negative bacteria and broader spectrum antibiotics when these genes are homologous to certain genes of Gram-positive bacteria.

15

- Screening of the bank for different phenotypes.

For the screening, knowledge of the sequence of each insertion is applied. For this, the mutants are organized into pools of 48. For each mutant, the insertion sites are amplified using suitable oligonucleotides. Each
20 amplification product is deposited on a nylon membrane. The pools of 48 mutants are then placed in the conditions for which mutants are sought. The total DNA is prepared using bacteria obtained from each output pool and an amplification is carried out using oligonucleotides which served to amplify the 48 insertion sites. The amplification product then serves to hybridize the
25 membranes which correspond to each pool. The mutants for which no amplification is detected are mutants for the phenotype considered.

- Search for mutants important for growth in serum

As mentioned above, *N. meningitidis* is a bacteria having extracellular
30 multiplication perfectly suited to this compartment. The invention therefore related to identifying in an exhaustive way the attributes and the genes required for this growth.

1 - solation of the strains:

The wild strain 2C43 wt (positive control) and Z5463 CPS- (non-capsulated strain, negative control) are isolated on a GCB plate (agar 5g/1); the mutants produced from the strain 8013 are isolated on a GCB plate + *Kanamycin* 100 µg/pl.

5 The culture is carried out over 14 – 18 hours, at 37°C, in 5% CO₂.

2-Serum:

10 The complemented human serum is stored at -80°C. After heating for 30 min. at 56°C, the serum is decomplexed. Growth is produced for the controls and the mutants with systematically complemented and decomplexed serum.

Each mutant is tested with a positive and a negative control to compare the growth curves produced on different days.

15

3-Inoculum:

20 1 dose of well-isolated colonies is collected and dissociated in 5 ml of RPMI (GIBCO: RPMI 1640 medium with glutamax I; previously placed for 5-10 min. at ambient temperature before inoculation, to protect the bacteria from rapid variations at temperature). The mass of bacteria is taken up using a P1000, then vortexed. The preculture is subjected to stirring at 37 °C for 2 hours. The OD is then measured at 600 nm (the white control being RMPI) and the inoculum is returned to 0.1 in RPMI (previously placed for 5-10 min. at ambient temperature).

25

4-Growth medium:

98 µl of serum and 292 µl of RPMI (25% serum, 75% RMPI) is deposited per well and left for 5 min. at ambient temperature before inoculation.

30

400 µl of water is introduced into the optionally empty wells.

5-Inoculation:

After stirring, 10 µl of inoculum adjusted to 0.1 of OD is collected, and it is deposited in a well containing growth medium, then mixed using a P1000. The well is placed in an oven at 37°C, in 5% CO₂. The inoculum is analyzed at T0 and the bacterial growth at various times, by plating 50 µl of different dilutions on GCB plates.

6-Sampling:

Suspension takes place again (with a P1000) before sampling at 0 hour, 1 hour, 5 hours post inoculation. 20 µl of inoculated culture medium is taken which is placed in 180 µl of RPMI (D1; tube 1.5 ml, previously placed at ambient temperature for 10 min., before sampling, in order to avoid a large difference in temperature). The mixture is vortexed.

7-Dilutions:

The tube D1 is vortexed, then 50 µl of D1 is sampled which is added to 450 µl of RPMI (D2; 2 ml tube, previously placed at ambient temperature for 10 min.). Between each dilution stage vortexing is carried out and the cone is changed. Dilutions are carried out up to the dilution D4 for the time T0, D3 for the time T1, and D5 for the time T5.

8-Inoculation:

The inoculation takes place on a GCB plate for the controls, and GCB+ kanamycin 100 µg/µl for the mutants. Vortexing is carried out, then 50 µl is taken from each dilution, followed by incubating upside down in an oven at 37°C, in 5% CO₂, for 14-18 hours, before counting the colonies. D4, 3 are inoculated for the time T0; D0, 1, 2, 3 for the time T1; D5, 4, 3, 2, 1 for the time T5.

9-Genes of Nm allowing growth in serum: counting the surviving bacteria in serum as a function of time

A growth curve representing the number of bacteria surviving in the serum as a function of time was drawn up for each of the clones (log₁₀ CFU as a function of incubation time in hours).

Two control strains were included each time in the test: the wild strain corresponding to a strain of *Neisseria meningitidis*, serogroup C and a control strain corresponding to *Neisseria meningitidis*, serogroup A without capsule. For each gene a single mutant is represented.

5

The results are given in Figures 4 to 24, which represent the growth curves of the mutants of Figure 3 in the complemented serum and the de complemented serum.

10

- Identification of the adhesins for endothelial cells.

The important adhesins for interaction on endothelial cells can be used to allow the opening of the blood-brain barrier and to allow medicaments to pass into the brain.

15

HUVEC cells at confluence are inoculated in 24-well cell culture microplates at a density of 10^5 /well. The cells are washed the following day in 10% serum/RPMI, and are incubated for 2 hours at 37°C. At the same time, the bacteria are resuspended in the same medium at an OD₅₅₀ of 0.1 to 0.01 and incubated for 2 hours at 37°C. The suspension of bacteria is used to infect the cells for 30 min at 37°C.

20

The infection then continues for 4-5 hours with the cells being washed each hour.

CLAIMS

1/ Exhaustive method for detecting pathogenic bacteria genes, in particular Nm, expressing a desired phenotype, characterized in that :

- a bank of mutants generated from a given bacterial strain is used so that at least 70% of the non-essential genes, and in particular at least 80%, or even more than 90%, are mutagenized by inserting a transposon in a reading frame,

- the mutants are then brought into contact, either individually, or in pools, with an environment, such as a medium, an animal or cells, capable of interacting with the mutant bacteria expressing the desired phenotype,

- when pools are used, the bacteria not having reacted with the desired phenotype are recovered,

- the mutated genes of these bacteria are identified and their involvement in said phenotype is verified.

2/ Method according to claim 1, characterized in that, in the contact stage, the mutants of the bank are passed through serum.

3/ Method according to claim 1, characterized in that, in the contact stage, the mutants of the bank are passed over endothelial cells.

4/ Genes which give a bacteria the ability to grow or to interact with a given environment, such as serum, an *in vivo* animal model, cells, characterized in that they can be obtained by the method according to any one of claims 1 to 3.

5/ Genes according to claim 4, characterized in that they are involved in the growth of the bacteria in serum and are chosen from those in Figure 3.

6/ Genes according to claim 5, characterized in that they are chosen from Nm 83 dxr, Nm 229, Nm 356, Nm 848 galU, and the genes of serogroup B, Nm B 1771 and Nm B 65.

7/ Genes according to claim 4, characterized in that they are involved in the interaction with endothelial cells.

8/ Application of the genes selected according to the method of claim 2, or according to claim 5 or 6, as anti-pathogenicity targets, which consists in inhibiting Nm growth *in vivo* in the serum.

CLAIMS

1/ Exhaustive method for detecting pathogenic bacteria genes, in particular Nm, expressing a desired phenotype, characterized in that :

5 - a bank of mutants generated from a given bacterial strain is used so that at least 70% of the non-essential genes, and in particular at least 80%, or even more than 90%, are mutagenized by inserting a transposon in a reading frame,

10 - the mutants are then brought into contact, either individually, or in pools, with an environment, such as a medium, an animal or cells, capable of interacting with the mutant bacteria expressing the desired phenotype,

 - when pools are used, the bacteria not having reacted with the desired phenotype are recovered,

 - the mutated genes of these bacteria are identified and their involvement in said phenotype is verified.

15 2/ Method according to claim 1, characterized in that, in the contact stage, the mutants of the bank are passed through serum.

 3/ Method according to claim 1, characterized in that, in the contact stage, the mutants of the bank are passed over endothelial cells.

20 4/ Nm genes, characterized in that they are chosen from dxr (1-deoxy-D-xylulose-5-phosphate reductoisomerase), galU (UTP-glucose-1-phosphate uridylyltransferase), and the gene of serotype B hisC (histidinol-phosphate amino transferase).

25 5/ Application of the genes selected according to the method of claim 2, or according to claim 4, as anti-pathogenicity targets, which consists of inhibiting the growth of Nm in serum.

30 6/ Application of the genes selected according to the method of claim 3, or according to claim 4, for the screening and manufacture of medicaments allowing the opening of the blood-brain barrier to therapeutic ingredients such as medicaments for Parkinson's Disease, Alzheimer's disease, antimitotics, medicaments for multiple sclerosis, antivirals, antimycotics and antibiotics.

 7/ Application according to one of claims 5 or 6, of the essential genes of Nm as targets for the screening and manufacture of antibiotics.

CLAIMS

1/ Exhaustive method for detecting pathogenic bacteria genes, in particular Nm, expressing a desired phenotype, characterized in that :

5 - a bank of mutants generated from a given bacterial strain is used so that at least 70% of the non-essential genes, and in particular at least 80%, or even more than 90%, are mutagenized by inserting a transposon in a reading frame,

10 - the mutants are then brought into contact, either individually, or in pools, with an environment, such as a medium, an animal or cells, capable of interacting with the mutant bacteria expressing the desired phenotype,

 - when pools are used, the bacteria not having reacted with the desired phenotype are recovered,

 - the mutated genes of these bacteria are identified and their involvement in said phenotype is verified.

15 2/ Method according to claim 1, characterized in that, in the contact stage, the mutants of the bank are passed through serum.

 3/ Method according to claim 1, characterized in that, in the contact stage, the mutants of the bank are passed over endothelial cells.

9/ Application of the genes selected according to the method of claim 3, or according to claim 7, to allow the opening of the blood-brain barrier to therapeutic ingredients such as medicaments for Parkinson's Disease, Alzheimer's disease, antimitotics, medicaments for multiple sclerosis, 5 antivirals, antimycotics and antibiotics.

10/ Application of the essential genes of Nm as targets for developing antibiotics.

Z2491 orfs having more than 65 % homology with MC58

Z2491 gene	MC58 in silico
NMA0002	99
NMA0003	99
NMA0004	100
NMA0005	100
NMA0006	99
NMA0007	99
NMA0008	100
NMA0009	99
NMA0010	97
NMA0011	97
NMA0012	99
NMA0013	98
NMA0014	99
NMA0015	98
NMA0016	99
NMA0017	97
NMA0018	99
NMA0019	99
NMA0020	99
NMA0021	100
NMA0022	78
NMA0023	100
NMA0024	94
NMA0025	97
NMA0027	97
NMA0028	99
NMA0029	95
NMA0030	100
NMA0031	99
NMA0032	99
NMA0033	99
NMA0035	97
NMA0036	77
NMA0037	100
NMA0042	98
NMA0043	100
NMA0044	98
NMA0048	99
NMA0049	98
NMA0050	100
NMA0052	95
NMA0054	97
NMA0055	99
NMA0056	99
NMA0057	98
NMA0059	91
NMA0060	99
NMA0061	98
NMA0062	98
NMA0063	97
NMA0064	100

Figure 1

NMA0065	94
NMA0066	98
NMA0067	97
NMA0068	88
NMA0069	98
NMA0070	99
NMA0071	99
NMA0072	99
NMA0073	100
NMA0074	99
NMA0075	98
NMA0076	97
NMA0077	98
NMA0078	96
NMA0079	99
NMA0080	100
NMA0081	99
NMA0082	99
NMA0083	98
NMA0084	99
NMA0085	99
NMA0086	98
NMA0087	98
NMA0088	99
NMA0090	99
NMA0091	98
NMA0092	98
NMA0093	99
NMA0094	98
NMA0096	70
NMA0098	99
NMA0099	98
NMA0100	99
NMA0101	99
NMA0102	99
NMA0103	100
NMA0104	100
NMA0105	100
NMA0106	100
NMA0107	97
NMA0108	100
NMA0109	99
NMA0110	99
NMA0111	100
NMA0112	100
NMA0113	100
NMA0114	99
NMA0115	100
NMA0116	100
NMA0117	99
NMA0118	100
NMA0119	100
NMA0120	100
NMA0121	100
NMA0122	100
NMA0123	100

Figure 1 (cntd)

NMA0124	100	Figure 1 (cntd)
NMA0125	100	
NMA0126	99	
NMA0127	97	
NMA0128	100	
NMA0129	100	
NMA0133	100	
NMA0134	100	
NMA0135	99	
NMA0136	100	
NMA0137	100	
NMA0138	95	
NMA0139	98	
NMA0140	83	
NMA0141	99	
NMA0142	99	
NMA0143	100	
NMA0144	99	
NMA0145	100	
NMA0146	99	
NMA0147	100	
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NMA0196	88
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NMA0217	97
NMA0218	99
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NMA0221	96
NMA0222	99
NMA0224	99
NMA0225	99
NMA0226	99
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NMA0229	96
NMA0230	98
NMA0233	100
NMA0235	99
NMA0236	99
NMA0237	99
NMA0238	99
NMA0239	99
NMA0240	99
NMA0241	96
NMA0242	97
NMA0243	97
NMA0244	96
NMA0245	97
NMA0246	98
NMA0247	98
NMA0248	96
NMA0249	97
NMA0250	97
NMA0251	94

Figure 1 (cntd)

NMA0252	100	
NMA0253	98	
NMA0254	99	
NMA0255	98	
NMA0256	97	Figure 1 (cntd)
NMA0257	98	
NMA0258	99	
NMA0259	97	
NMA0260	98	
NMA0261	97	
NMA0262	97	
NMA0263	99	
NMA0264	91	
NMA0265	90	
NMA0266	86	
NMA0267	87	
NMA0268	86	
NMA0269	86	
NMA0270	83	
NMA0271	66	
NMA0272	66	
NMA0273	98	
NMA0274	95	
NMA0275	98	
NMA0276	98	
NMA0277	95	
NMA0279	98	
NMA0280	98	
NMA0281	99	
NMA0282	99	
NMA0283	98	
NMA0284	97	
NMA0285	96	
NMA0286	91	
NMA0287	99	
NMA0288	99	
NMA0289	100	
NMA0290	99	
NMA0291	98	
NMA0292	98	
NMA0293	85	
NMA0295	99	
NMA0296	98	
NMA0298	98	
NMA0299	83	
NMA0300	96	
NMA0301	100	
NMA0303	99	
NMA0304	97	
NMA0305	99	
NMA0305A	98	
NMA0306	100	
NMA0307	98	
NMA0308	98	
NMA0309	100	
NMA0310	100	

NMA0311	100	Figure 1 (cntd)
NMA0312	99	
NMA0313	96	
NMA0314	100	
NMA0315	94	
NMA0316	100	
NMA0317	100	
NMA0318	100	
NMA0319	96	
NMA0320	100	
NMA0321	99	
NMA0322	99	
NMA0323	100	
NMA0324	75	
NMA0325	100	
NMA0326	100	
NMA0327	100	
NMA0328	100	
NMA0329	94	
NMA0330	88	
NMA0331	98	
NMA0333	99	
NMA0335	92	
NMA0336	100	
NMA0337	99	
NMA0338	94	
NMA0339	97	
NMA0340	100	
NMA0341	99	
NMA0342	98	
NMA0343	96	
NMA0344	98	
NMA0344A	100	
NMA0345	98	
NMA0346	100	
NMA0347	98	
NMA0348	100	
NMA0349	94	
NMA0350	98	
NMA0351	97	
NMA0353	97	
NMA0354	100	
NMA0356	98	
NMA0357	98	
NMA0358	91	
NMA0360	100	
NMA0361	99	
NMA0362	99	
NMA0363	97	
NMA0364	97	
NMA0365	89	
NMA0366	80	
NMA0367	99	
NMA0368	95	
NMA0369	98	
NMA0370	99	

NMA0371	95
NMA0372	98
NMA0373	97
NMA0374	98
NMA0375	100
NMA0376	99
NMA0377	100
NMA0378	100
NMA0379	100
NMA0380	100
NMA0381	99
NMA0382	99
NMA0383	100
NMA0384	96
NMA0385	96
NMA0386	97
NMA0387	98
NMA0388	99
NMA0389	99
NMA0390	99
NMA0391	100
NMA0392	99
NMA0393	95
NMA0394	94
NMA0395	70
NMA0396	83
NMA0397	98
NMA0398	93
NMA0400	100
NMA0401	100
NMA0402	98
NMA0403	97
NMA0404	98
NMA0405	99
NMA0409	97
NMA0410	99
NMA0411	98
NMA0412	100
NMA0413	99
NMA0414	99
NMA0415	100
NMA0416	99
NMA0417	100
NMA0418	99
NMA0419	100
NMA0420	100
NMA0421	100
NMA0422	98
NMA0423	97
NMA0424	99
NMA0425	99
NMA0426A	85
NMA0430	95
NMA0431	98
NMA0433	99
NMA0434	100

Figure 1 (cntd)

NMA0435	100	
NMA0436	99	
NMA0437	98	
NMA0438	99	
NMA0439	100	Figure 1 (cntd)
NMA0440	89	
NMA0441	99	
NMA0442	99	
NMA0444	95	
NMA0445	98	
NMA0447	99	
NMA0448	94	
NMA0449	78	
NMA0450	98	
NMA0451	97	
NMA0452	99	
NMA0453	98	
NMA0454	99	
NMA0455	97	
NMA0456	97	
NMA0457	92	
NMA0458	95	
NMA0459	99	
NMA0461	96	
NMA0462	98	
NMA0463	99	
NMA0464	97	
NMA0465	98	
NMA0466	97	
NMA0467	96	
NMA0468	98	
NMA0470	99	
NMA0471	98	
NMA0472	99	
NMA0473	99	
NMA0476	98	
NMA0477	97	
NMA0478	97	
NMA0480	99	
NMA0483	98	
NMA0485	99	
NMA0486	100	
NMA0487	100	
NMA0488	98	
NMA0489	89	
NMA0490	99	
NMA0491	100	
NMA0492	100	
NMA0493	97	
NMA0494	95	
NMA0495	100	
NMA0496	97	
NMA0497	98	
NMA0498	99	
NMA0499	99	
NMA0501	98	

NMA0502	100
NMA0503	98
NMA0504	98
NMA0505	97
NMA0506	99
NMA0507	98
NMA0508	99
NMA0510	97
NMA0511	99
NMA0512	99
NMA0513	100
NMA0514	100
NMA0515	99
NMA0516	98
NMA0517	99
NMA0518	99
NMA0519	99
NMA0520	97
NMA0521	100
NMA0522	96
NMA0523	97
NMA0524	94
NMA0525	92
NMA0526	78
NMA0527	82
NMA0528	98
NMA0529	99
NMA0530	100
NMA0531	92
NMA0532	98
NMA0532a	95
NMA0533	98
NMA0534	98
NMA0535	99
NMA0536	97
NMA0537	94
NMA0538	98
NMA0541	100
NMA0542	98
NMA0543	98
NMA0544	98
NMA0545	98
NMA0546	98
NMA0547	96
NMA0548	98
NMA0549	99
NMA0550	97
NMA0551	100
NMA0552	98
NMA0553	99
NMA0554	91
NMA0555	97
NMA0556	96
NMA0557	99
NMA0559	93
NMA0560	95

Figure 1 (cntd)

NMA0561	97
NMA0562	96
NMA0563	80
NMA0564	98
NMA0565	99
NMA0567	99
NMA0568	75
NMA0569	100
NMA0570	98
NMA0571	97
NMA0572	98
NMA0573	93
NMA0574	99
NMA0575	99
NMA0576	99
NMA0577	99
NMA0578	99
NMA0579	97
NMA0580	98
NMA0581	98
NMA0582	100
NMA0583	95
NMA0584	97
NMA0585	93
NMA0586	96
NMA0587	99
NMA0588	92
NMA0589	98
NMA0590	99
NMA0591	86
NMA0592	97
NMA0594	98
NMA0595	97
NMA0596	98
NMA0597	100
NMA0598	99
NMA0599	97
NMA0600	99
NMA0601	98
NMA0602	98
NMA0605	92
NMA0607	66
NMA0608	99
NMA0609	87
NMA0611	96
NMA0612	99
NMA0613	100
NMA0614	99
NMA0615	98
NMA0616	99
NMA0617	99
NMA0618	100
NMA0619	99
NMA0620	98
NMA0621	95
NMA0622	97

Figure 1 (cntd)

NMA0623	100
NMA0624	100
NMA0625	99
NMA0626	77
NMA0627	99
NMA0632	98
NMA0632a	92
NMA0633	96
NMA0634	91
NMA0635	98
NMA0636	97
NMA0637	97
NMA0638	95
NMA0639	95
NMA0643	97
NMA0644	96
NMA0645	99
NMA0646	97
NMA0647	96
NMA0648	100
NMA0650	99
NMA0651	100
NMA0652	100
NMA0653	100
NMA0654	98
NMA0655	100
NMA0656	98
NMA0658	100
NMA0659	100
NMA0660	99
NMA0661	99
NMA0662	99
NMA0663	98
NMA0664	99
NMA0664a	100
NMA0665	98
NMA0666	99
NMA0668	100
NMA0669	100
NMA0670	97
NMA0671	77
NMA0672	99
NMA0673	98
NMA0674	99
NMA0675	99
NMA0676	97
NMA0677	93
NMA0678	96
NMA0679	97
NMA0680	100
NMA0681	96
NMA0683	97
NMA0684	100
NMA0685	100
NMA0686	100
NMA0687	98

Figure 1 (cntd)

NMA0688	78
NMA0690	66
NMA0691	100
NMA0692	98
NMA0693	99
NMA0694	100
NMA0695	70
NMA0696	95
NMA0696A	98
NMA0697	100
NMA0698	99
NMA0699	99
NMA0700	99
NMA0701	99
NMA0702	99
NMA0703	99
NMA0704	99
NMA0706	94
NMA0707	97
NMA0708	96
NMA0709	98
NMA0710	99
NMA0711	99
NMA0712	96
NMA0714	100
NMA0715	98
NMA0716	99
NMA0717	97
NMA0718	99
NMA0719	98
NMA0720	96
NMA0721	97
NMA0722	100
NMA0723	98
NMA0724	98
NMA0725	99
NMA0726	93
NMA0728	99
NMA0729	99
NMA0730	100
NMA0731	97
NMA0732	98
NMA0733	91
NMA0734	92
NMA0735	99
NMA0736	97
NMA0737	98
NMA0738	99
NMA0739	100
NMA0740	98
NMA0741	99
NMA0742	100
NMA0744	100
NMA0745	100
NMA0746	98
NMA0747	99

Figure 1 (cntd)

NMA0748	98
NMA0749	99
NMA0750	99
NMA0751	98
NMA0752	97
NMA0753	99
NMA0754	99
NMA0755	99
NMA0756	99
NMA0757	100
NMA0758	98
NMA0759	97
NMA0760	98
NMA0761	95
NMA0762	98
NMA0763	99
NMA0764	100
NMA0765	100
NMA0766	98
NMA0767	98
NMA0768	99
NMA0769	95
NMA0770	98
NMA0771	68
NMA0774	81
NMA0775	75
NMA0776	75
NMA0777	92
NMA0778	86
NMA0779	83
NMA0780	84
NMA0781	79
NMA0784	88
NMA0786	70
NMA0788	87
NMA0789	97
NMA0790	99
NMA0791	98
NMA0792	99
NMA0793	98
NMA0794	98
NMA0795	100
NMA0796	98
NMA0797	99
NMA0798	100
NMA0799	100
NMA0800	98
NMA0801	99
NMA0802	91
NMA0803	98
NMA0804	98
NMA0805	100
NMA0806	99
NMA0807	99
NMA0808	98
NMA0810	99

Figure 1 (cntd)

NMA0811	99
NMA0812	99
NMA0813	100
NMA0814	100
NMA0815	100
NMA0816	98
NMA0817	98
NMA0818	99
NMA0819	97
NMA0820	99
NMA0821	92
NMA0822	93
NMA0823	98
NMA0824	96
NMA0825	99
NMA0826	99
NMA0827	99
NMA0828	96
NMA0829	98
NMA0830	98
NMA0831	98
NMA0832	98
NMA0833	99
NMA0835	99
NMA0836	98
NMA0837	98
NMA0838	98
NMA0839	98
NMA0840	96
NMA0841	99
NMA0842	100
NMA0843	99
NMA0844	99
NMA0845	90
NMA0846	88
NMA0847	99
NMA0848	98
NMA0849	93
NMA0850	98
NMA0851	98
NMA0852	97
NMA0853	77
NMA0855	91
NMA0856	93
NMA0857	79
NMA0858	97
NMA0859	99
NMA0860	94
NMA0861	98
NMA0862	98
NMA0864	98
NMA0865	97
NMA0866	98
NMA0867	96
NMA0868	98
NMA0869	97

Figure 1 (cntd)

NMA0870	99
NMA0871	99
NMA0872	99
NMA0873	99
NMA0874	100
NMA0875	98
NMA0876	99
NMA0877	99
NMA0878	100
NMA0879	98
NMA0880	99
NMA0881	98
NMA0882	100
NMA0884	99
NMA0885	99
NMA0886	100
NMA0887	98
NMA0888	99
NMA0889	99
NMA0890	94
NMA0891	99
NMA0892	98
NMA0894	97
NMA0895	99
NMA0896	97
NMA0897	97
NMA0899	99
NMA0900	99
NMA0902	99
NMA0903	98
NMA0904	99
NMA0905	97
NMA0906	96
NMA0907	97
NMA0908	98
NMA0909	98
NMA0911	98
NMA0912	99
NMA0913	99
NMA0914	100
NMA0915	98
NMA0916	97
NMA0917	98
NMA0918	99
NMA0919	97
NMA0925	99
NMA0927	99
NMA0928	98
NMA0929	99
NMA0930	100
NMA0931	100
NMA0932	99
NMA0933	98
NMA0937	96
NMA0938	100
NMA0939	99

Figure 1 (cntd)

NMA0940	98
NMA0941	92
NMA0942	97
NMA0943	97
NMA0944	92
NMA0945	99
NMA0946	98
NMA0947	99
NMA0948	99
NMA0950	98
NMA0951	99
NMA0952	98
NMA0953	97
NMA0954	96
NMA0955	97
NMA0956	99
NMA0957	97
NMA0958	99
NMA0959	97
NMA0960	97
NMA0961	100
NMA0962	99
NMA0963	98
NMA0964	99
NMA0965	100
NMA0966	98
NMA0967	94
NMA0968	98
NMA0969	99
NMA0970	100
NMA0971	96
NMA0972	98
NMA0973	100
NMA0974	100
NMA0975	98
NMA0976	98
NMA0977	99
NMA0978	95
NMA0979	99
NMA0980	92
NMA0981	98
NMA0982	97
NMA0983	70
NMA0984	100
NMA0985	99
NMA0986	96
NMA0987	97
NMA0988	96
NMA0989	99
NMA0990	97
NMA0991	98
NMA0992	98
NMA0993	98
NMA0994	99
NMA0995	98
NMA0996	99

Figure 1 (cntd)

NMA0997	98	Figure 1 (cntd)
NMA0999	99	
NMA1000	99	
NMA1001	97	
NMA1002	100	
NMA1003	99	
NMA1004	98	
NMA1005	100	
NMA1006	99	
NMA1007	99	
NMA1008	100	
NMA1009	97	
NMA1010	96	
NMA1011	99	
NMA1012	98	
NMA1013	98	
NMA1015	98	
NMA1016	98	
NMA1017	100	
NMA1018	98	
NMA1019	95	
NMA1020	98	
NMA1021	98	
NMA1022	98	
NMA1023	99	
NMA1024	97	
NMA1025	93	
NMA1026	99	
NMA1027	100	
NMA1028	99	
NMA1029	98	
NMA1030	99	
NMA1031	99	
NMA1032	99	
NMA1033	99	
NMA1034	97	
NMA1035	99	
NMA1036	90	
NMA1037	99	
NMA1038	98	
NMA1039	100	
NMA1042	93	
NMA1045	94	
NMA1046	39	
NMA1047	99	
NMA1048	98	
NMA1049	86	
NMA1051	91	
NMA1052	99	
NMA1053	97	
NMA1054	98	
NMA1056	99	
NMA1057	93	
NMA1058	89	
NMA1059	96	
NMA1060	100	

NMA1061	98
NMA1062	99
NMA1063	98
NMA1064	97
NMA1065	98
NMA1066	98
NMA1067	99
NMA1068	99
NMA1070	99
NMA1071	88
NMA1072	100
NMA1073	100
NMA1074	99
NMA1075	80
NMA1076	98
NMA1084	97
NMA1085	99
NMA1086	98
NMA1087	100
NMA1088	97
NMA1089	96
NMA1090	97
NMA1091	95
NMA1092	97
NMA1093	100
NMA1094	98
NMA1095	99
NMA1096	99
NMA1097	98
NMA1098	99
NMA1100	99
NMA1101	99
NMA1102	100
NMA1104	99
NMA1105	99
NMA1106	93
NMA1107	93
NMA1108	82
NMA1109	96
NMA1110	97
NMA1111	94
NMA1112	98
NMA1113	98
NMA1114	98
NMA1115	98
NMA1116	98
NMA1117	96
NMA1118	98
NMA1119	98
NMA1120	99
NMA1121	98
NMA1122	99
NMA1123	99
NMA1124	98
NMA1126	100
NMA1127	97

Figure 1 (cntd)

NMA1128	97	
NMA1129	98	
NMA1129a	98	
NMA1130	94	
NMA1131	98	Figure 1 (cntd)
NMA1132	97	
NMA1133	99	
NMA1134	94	
NMA1135	99	
NMA1136	98	
NMA1137	100	
NMA1138	98	
NMA1139	99	
NMA1140	98	
NMA1141	100	
NMA1142	99	
NMA1143	100	
NMA1144	98	
NMA1145	99	
NMA1146	100	
NMA1147	100	
NMA1148	100	
NMA1149	100	
NMA1150	96	
NMA1151	99	
NMA1152	100	
NMA1153	99	
NMA1154	99	
NMA1159	98	
NMA1160	98	
NMA1161	99	
NMA1162	95	
NMA1163	98	
NMA1164	100	
NMA1165	99	
NMA1166	100	
NMA1167	98	
NMA1168	96	
NMA1169	100	
NMA1170	99	
NMA1171	100	
NMA1172	74	
NMA1173	70	
NMA1174	100	
NMA1175	97	
NMA1176	92	
NMA1177	97	
NMA1178	97	
NMA1179	96	
NMA1180	98	
NMA1181	92	
NMA1182	96	
NMA1183	98	
NMA1185	94	
NMA1186	88	
NMA1187	100	

NMA1188	97
NMA1189	99
NMA1190	97
NMA1191	96
NMA1192	100
NMA1193	100
NMA1194	100
NMA1195	100
NMA1196	95
NMA1197	97
NMA1198	100
NMA1199	98
NMA1200	90
NMA1201	100
NMA1202	98
NMA1203	100
NMA1204	100
NMA1205	98
NMA1206	98
NMA1207	95
NMA1208	94
NMA1212	94
NMA1217	93
NMA1218	97
NMA1219	96
NMA1220	98
NMA1221	98
NMA1222	99
NMA1223	100
NMA1224	99
NMA1230	100
NMA1231	100
NMA1232	90
NMA1233	97
NMA1234	82
NMA1237	99
NMA1239	79
NMA1242	84
NMA1243	99
NMA1244	99
NMA1245	97
NMA1246	98
NMA1247	99
NMA1249	98
NMA1250	99
NMA1251	99
NMA1252	98
NMA1253	98
NMA1254	99
NMA1255	99
NMA1256	90
NMA1257	99
NMA1258	100
NMA1259	97
NMA1260	98
NMA1261	96

Figure 1 (cntd)

NMA1262	99	Figure 1 (cntd)
NMA1263	98	
NMA1264	95	
NMA1265	98	
NMA1266	97	
NMA1267	98	
NMA1268	98	
NMA1270	99	
NMA1272	99	
NMA1273	98	
NMA1274	98	
NMA1275	99	
NMA1276	99	
NMA1278	98	
NMA1279	98	
NMA1280	96	
NMA1281	96	
NMA1284	94	
NMA1285	72	
NMA1286	83	
NMA1301	88	
NMA1302	100	
NMA1303	97	
NMA1304	99	
NMA1305	97	
NMA1306	95	
NMA1307	83	
NMA1308	83	
NMA1309	66	
NMA1310	98	
NMA1311	70	
NMA1312	86	
NMA1313	97	
NMA1314	99	
NMA1315	99	
NMA1316	100	
NMA1318	99	
NMA1319	99	
NMA1320	98	
NMA1321	100	
NMA1322	97	
NMA1323	99	
NMA1324	98	
NMA1325	96	
NMA1326	100	
NMA1327	98	
NMA1328	97	
NMA1329	97	
NMA1330	98	
NMA1331	98	
NMA1332	100	
NMA1334	100	
NMA1335	100	
NMA1336	94	
NMA1338	98	
NMA1339	98	

NMA1340	98
NMA1341	99
NMA1343	97
NMA1344	100
NMA1345	91
NMA1347	100
NMA1348	100
NMA1349	99
NMA1350	99
NMA1351	99
NMA1353	100
NMA1354	100
NMA1355	90
NMA1356	96
NMA1357	96
NMA1358	99
NMA1359	96
NMA1360	98
NMA1361	98
NMA1362	99
NMA1363	95
NMA1364	99
NMA1365	99
NMA1366	94
NMA1367	95
NMA1368	97
NMA1369	96
NMA1370	99
NMA1371	98
NMA1372	99
NMA1373	100
NMA1374	98
NMA1375	100
NMA1376	100
NMA1377	99
NMA1378	99
NMA1379	99
NMA1380	100
NMA1381	99
NMA1382	99
NMA1383	96
NMA1384	98
NMA1385	96
NMA1390	100
NMA1391	96
NMA1393	95
NMA1394	98
NMA1395	100
NMA1396	95
NMA1397	99
NMA1398	98
NMA1400	98
NMA1401	99
NMA1402	99
NMA1403	98
NMA1404	98

Figure 1 (cntd)

NMA1405	100
NMA1406	99
NMA1407	99
NMA1408	98
NMA1409	99
NMA1410	99
NMA1411	99
NMA1412	98
NMA1413	98
NMA1414	97
NMA1415	98
NMA1416	98
NMA1417	98
NMA1418	97
NMA1419	100
NMA1420	99
NMA1421	99
NMA1423	96
NMA1424	93
NMA1425	98
NMA1427	97
NMA1429	98
NMA1430	90
NMA1432	99
NMA1433	98
NMA1437	100
NMA1438	99
NMA1439	97
NMA1440	97
NMA1441	98
NMA1442	100
NMA1443	100
NMA1444	99
NMA1445	98
NMA1446	99
NMA1447	99
NMA1448	98
NMA1449	98
NMA1450	99
NMA1451	100
NMA1452	99
NMA1453	98
NMA1454	98
NMA1456	98
NMA1457	98
NMA1459	99
NMA1460	98
NMA1461	100
NMA1462	99
NMA1463	99
NMA1464	96
NMA1465	98
NMA1466	97
NMA1468	99
NMA1469	96
NMA1470	97

Figure 1 (cntd)

NMA1471	99	Figure 1 (cntd)
NMA1472	98	
NMA1473	98	
NMA1474	98	
NMA1475	96	
NMA1476	97	
NMA1478	98	
NMA1479	97	
NMA1480	100	
NMA1481	99	
NMA1482	98	
NMA1483	99	
NMA1484	99	
NMA1485	99	
NMA1486	99	
NMA1487	90	
NMA1488	99	
NMA1489	95	
NMA1490	99	
NMA1491	87	
NMA1492	99	
NMA1493	98	
NMA1494	96	
NMA1495	99	
NMA1496	100	
NMA1497	100	
NMA1498	99	
NMA1499	99	
NMA1500	100	
NMA1501	99	
NMA1503	96	
NMA1504	99	
NMA1505	98	
NMA1506	99	
NMA1507	98	
NMA1508	100	
NMA1509	97	
NMA1514	98	
NMA1515	99	
NMA1516	100	
NMA1517	100	
NMA1518	100	
NMA1519	99	
NMA1520	100	
NMA1521	100	
NMA1522	99	
NMA1523	99	
NMA1524	98	
NMA1525	98	
NMA1526	99	
NMA1527	98	
NMA1528	99	
NMA1529	99	
NMA1531	99	
NMA1532	100	
NMA1533	93	

NMA1534	99
NMA1535	100
NMA1536	99
NMA1537	99
NMA1538	99
NMA1539	96
NMA1540	98
NMA1541	97
NMA1542	98
NMA1543	98
NMA1545	98
NMA1546	99
NMA1547	99
NMA1548	98
NMA1549	99
NMA1550	97
NMA1551	99
NMA1552	98
NMA1553	98
NMA1554	99
NMA1555	99
NMA1556	97
NMA1557	99
NMA1558	77
NMA1559	99
NMA1560	99
NMA1561	93
NMA1562	99
NMA1563	96
NMA1564	100
NMA1565	98
NMA1566	98
NMA1567	95
NMA1568	98
NMA1569	99
NMA1570	98
NMA1571	96
NMA1572	99
NMA1573	98
NMA1574	99
NMA1575	96
NMA1576	98
NMA1577	98
NMA1578	97
NMA1579	98
NMA1580	99
NMA1581	98
NMA1582	99
NMA1583	93
NMA1584	97
NMA1585	99
NMA1586	98
NMA1588	96
NMA1589	96
NMA1591	93
NMA1592	99

Figure 1 (cntd)

NMA1593	100
NMA1594	96
NMA1595	99
NMA1596	98
NMA1597	100
NMA1598	99
NMA1599	99
NMA1600	99
NMA1601	100
NMA1601a	99
NMA1601b	98
NMA1602	99
NMA1603	97
NMA1604	99
NMA1605	100
NMA1607	100
NMA1608	100
NMA1609	98
NMA1610	98
NMA1611	100
NMA1612	92
NMA1613	98
NMA1614	99
NMA1615	99
NMA1616	100
NMA1617	99
NMA1618	95
NMA1619	98
NMA1620	99
NMA1621	100
NMA1622	99
NMA1623	99
NMA1624	99
NMA1625	85
NMA1626	86
NMA1627	98
NMA1628	97
NMA1629	99
NMA1630	98
NMA1631	99
NMA1632	100
NMA1633	97
NMA1634	99
NMA1635	99
NMA1636	91
NMA1637	81
NMA1638	99
NMA1639	100
NMA1640	98
NMA1641	94
NMA1642	97
NMA1643	99
NMA1644	96
NMA1645	100
NMA1646	98
NMA1647	98

Figure 1 (cntd)

NMA1648	99	
NMA1649	96	
NMA1650	99	
NMA1651	99	
NMA1652	91	Figure 1 (cntd)
NMA1653	98	
NMA1654	99	
NMA1655	97	
NMA1656	95	
NMA1657	99	
NMA1658	99	
NMA1659	98	
NMA1660	98	
NMA1661	98	
NMA1662	98	
NMA1663	93	
NMA1664	99	
NMA1665	98	
NMA1666	91	
NMA1667	99	
NMA1668	99	
NMA1669	99	
NMA1670	99	
NMA1671	99	
NMA1672	100	
NMA1673	98	
NMA1674	99	
NMA1675	98	
NMA1676	88	
NMA1677	89	
NMA1678	99	
NMA1679	99	
NMA1680	99	
NMA1681	91	
NMA1682	97	
NMA1683	99	
NMA1684	99	
NMA1685	100	
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NMA1688	100	
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NMA1691	98	
NMA1692	96	
NMA1693	97	
NMA1694	99	
NMA1695	98	
NMA1696	96	
NMA1697	95	
NMA1698	99	
NMA1699	99	
NMA1700	98	
NMA1701	99	
NMA1702	99	
NMA1703	99	

NMA1704	99
NMA1705	97
NMA1706	98
NMA1707	98
NMA1708	99
NMA1709	100
NMA1710	100
NMA1711	99
NMA1712	99
NMA1713	99
NMA1714	94
NMA1715	99
NMA1716	99
NMA1717	100
NMA1718	99
NMA1719	99
NMA1720	99
NMA1721	97
NMA1722	100
NMA1723	93
NMA1724	97
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NMA1727	98
NMA1728	95
NMA1729	93
NMA1730	98
NMA1731	100
NMA1732	95
NMA1733	97
NMA1734	99
NMA1735	99
NMA1736	97
NMA1737	99
NMA1738	94
NMA1739	97
NMA1740	83
NMA1741	98
NMA1742	99
NMA1743	99
NMA1744	96
NMA1745	97
NMA1746	97
NMA1747	95
NMA1748	98
NMA1749	97
NMA1750	97
NMA1751	100
NMA1752	99
NMA1753	99
NMA1754	100
NMA1755	97
NMA1756	99
NMA1757	99
NMA1758	98
NMA1759	98

Figure 1 (cntd)

NMA1760	99
NMA1761	99
NMA1762	99
NMA1763	99
NMA1764	99
NMA1765	100
NMA1766	99
NMA1767	99
NMA1768	100
NMA1769	100
NMA1770	99
NMA1771	98
NMA1772	100
NMA1773	99
NMA1774	91
NMA1775	97
NMA1776	97
NMA1777	94
NMA1778	99
NMA1779	97
NMA1780	97
NMA1781	99
NMA1782	99
NMA1783	100
NMA1784	98
NMA1785	99
NMA1786	99
NMA1788	97
NMA1792	99
NMA1793	98
NMA1794	99
NMA1795	95
NMA1796	100
NMA1797	93
NMA1798	98
NMA1799	97
NMA1800	99
NMA1801	99
NMA1802	98
NMA1803	95
NMA1805	100
NMA1806	99
NMA1807	100
NMA1808	98
NMA1809	95
NMA1810	98
NMA1811	98
NMA1812	99
NMA1813	99
NMA1814	99
NMA1815	98
NMA1816	98
NMA1817	99
NMA1818	98
NMA1819	98
NMA1820	100

Figure 1 (cntd)

NMA1828	67
NMA1851	66
NMA1852	93
NMA1854	84
NMA1858	100
NMA1859	100
NMA1860	98
NMA1861	95
NMA1862	97
NMA1863	99
NMA1864	96
NMA1866	77
NMA1868	80
NMA1883	73
NMA1884	84
NMA1886	98
NMA1887	98
NMA1888	91
NMA1890	84
NMA1891	100
NMA1892	100
NMA1894	99
NMA1895	100
NMA1896	99
NMA1897	98
NMA1898	93
NMA1899	97
NMA1900	98
NMA1901	99
NMA1902	99
NMA1903	98
NMA1904	99
NMA1905	99
NMA1906	98
NMA1907	99
NMA1907A	100
NMA1908	98
NMA1909	99
NMA1911	97
NMA1912	99
NMA1913	98
NMA1914	95
NMA1915	98
NMA1916	93
NMA1917	98
NMA1918	100
NMA1919	99
NMA1920	99
NMA1921	97
NMA1922	97
NMA1923	98
NMA1925	96
NMA1927	97
NMA1928	98
NMA1929	100
NMA1930	99

Figure 1 (cntd)

NMA1931	97
NMA1932	100
NMA1933	94
NMA1934	99
NMA1935	95
NMA1936	99
NMA1937	98
NMA1938	94
NMA1939	99
NMA1940	97
NMA1941	99
NMA1942	98
NMA1943	97
NMA1944	99
NMA1945	99
NMA1946	84
NMA1947	93
NMA1948	89
NMA1949	98
NMA1950	92
NMA1951	96
NMA1952	98
NMA1953	96
NMA1954	97
NMA1955	98
NMA1956	98
NMA1957	98
NMA1958	99
NMA1959	98
NMA1960	93
NMA1961	99
NMA1962	99
NMA1963	99
NMA1964	99
NMA1965	98
NMA1966	97
NMA1967	97
NMA1968	98
NMA1969	99
NMA1970	97
NMA1971	99
NMA1972	98
NMA1973	99
NMA1974	96
NMA1975	97
NMA1976	98
NMA1977	99
NMA1978	100
NMA1979	99
NMA1980	100
NMA1981	98
NMA1982	99
NMA1983	100
NMA1984	100
NMA1985	99
NMA1986	99

Figure 1 (cntd)

NMA1987	99
NMA1988	100
NMA1989	99
NMA1990	100
NMA1991	96
NMA1992	92
NMA1994	99
NMA1995	95
NMA1996	95
NMA1997	99
NMA1998	99
NMA1999	98
NMA2000	96
NMA2001	100
NMA2002	99
NMA2003	100
NMA2004	99
NMA2005	100
NMA2006	100
NMA2007	100
NMA2008	100
NMA2009	100
NMA2010	99
NMA2011	96
NMA2012	97
NMA2013	98
NMA2014	99
NMA2015	99
NMA2016	100
NMA2017	99
NMA2018	97
NMA2019	98
NMA2020	99
NMA2021	97
NMA2022	100
NMA2023	99
NMA2024	97
NMA2025	82
NMA2026	100
NMA2027	99
NMA2028	97
NMA2030	97
NMA2031	100
NMA2032	98
NMA2033	97
NMA2034	97
NMA2035	99
NMA2036	98
NMA2037	98
NMA2038	97
NMA2039	98
NMA2040	99
NMA2041	98
NMA2043	81
NMA2044	96
NMA2045	99

Figure 1 (cntd)

NMA2046	99
NMA2047	98
NMA2048	99
NMA2049	99
NMA2050	99
NMA2051	99
NMA2052	98
NMA2053	99
NMA2054	100
NMA2055	99
NMA2056	99
NMA2057	100
NMA2058	99
NMA2059	99
NMA2060	98
NMA2061	99
NMA2062	98
NMA2063	99
NMA2064	96
NMA2065	69
NMA2066	99
NMA2067	96
NMA2068	98
NMA2069	94
NMA2071	98
NMA2072	100
NMA2073	100
NMA2074	98
NMA2075	98
NMA2076	98
NMA2077	98
NMA2078	97
NMA2079	96
NMA2080	98
NMA2081	98
NMA2083	100
NMA2084	93
NMA2085	97
NMA2086	96
NMA2087	91
NMA2088	98
NMA2089	99
NMA2090	98
NMA2091	99
NMA2092	97
NMA2093	96
NMA2094	96
NMA2097	96
NMA2098	97
NMA2099	99
NMA2100	99
NMA2101	99
NMA2102	99
NMA2103	97
NMA2105	98
NMA2106	99

Figure 1 (cntd)

NMA2107	100
NMA2108	99
NMA2109	100
NMA2111	99
NMA2112	98
NMA2113	69
NMA2114	85
NMA2115	69
NMA2117	99
NMA2118	95
NMA2120	97
NMA2122	99
NMA2123	98
NMA2124	99
NMA2126	98
NMA2127	98
NMA2128	98
NMA2129	98
NMA2130	99
NMA2131	98
NMA2132	100
NMA2133	99
NMA2134	96
NMA2135	98
NMA2136	96
NMA2137	97
NMA2138	96
NMA2139	97
NMA2140	96
NMA2141	98
NMA2142	100
NMA2143	97
NMA2144	99
NMA2145	100
NMA2146	97
NMA2147	100
NMA2148	98
NMA2149	98
NMA2150	99
NMA2151	98
NMA2152	99
NMA2153	99
NMA2154	95
NMA2155	100
NMA2156	98
NMA2157	99
NMA2158	98
NMA2159	100
NMA2160	99
NMA2161	100
NMA2162	100
NMA2163	100
NMA2164	98
NMA2165	100
NMA2166	100
NMA2167	99

Figure 1 (cntd)

NMA2168	99
NMA2169	100
NMA2170	98
NMA2171	97
NMA2172	99
NMA2173	96
NMA2174	99
NMA2175	96
NMA2176	100
NMA2177	99
NMA2178	99
NMA2179	99
NMA2180	99
NMA2181	83
NMA2182	99
NMA2183	96
NMA2184	97
NMA2185	97
NMA2186	99
NMA2187	98
NMA2188	94
NMA2189	98
NMA2190	98
NMA2191	100
NMA2193	99
NMA2195	99
NMA2196	100
NMA2197	98
NMA2198	89
NMA2199	96
NMA2200	97
NMA2201	99
NMA2202	100
NMA2203	99
NMA2204	99
NMA2205	98
NMA2206	97
NMA2207	98
NMA2208	98
NMA2209	99
NMA2210	97
NMA2211	96
NMA2212	97
NMA2213	98
NMA2214	98
NMA2215	97
NMA2216	100
NMA2217	98
NMA2218	99
NMA2219	96
NMA2220	85
NMA2221	98
NMA2222	100
NMA2223	98
NMA2224	98
NMA2225	95

Figure 1 (cntd)

NMA2226
NMA2227
NMA2228
NMA2229

96
94
96
98

Figure 1 (cntd)

515 Genes mutated on 29/11/01

Figure 2A

The mutants in red present an increased sensitivity to the bactericidal action of the complement of human serum.

Nm2: *nuoL*, NADH dehydrogenase I chain L 8/1
Nm3: unknown 35/25
Nm10: *nuoG*, NADH dehydrogenase I chain G 16/33, 26/39
Nm15: *nuoE*, NADH dehydrogenase I chain E 8/41
Nm17: *nuoC*, NADH dehydrogenase I chain C 29/44, 57/25
Nm18: *nuoB*, NADH dehydrogenase I chain B 7/39', 64/45'
Nm20: probable integral membrane protein 20/44
Nm22: possible transposase for IS1016 9/17
Nm24: unknown 20/7
Nm29: unknown 93/8
Nm37: unknown 95/37
Nm39: unknown 5/31, 24/16', 53/27', 93/13
Nm42: *pyrD*, dihydroorotate dehydrogenase 79/39
Nm47: probable transmembrane transport protein 71/19
Nm48: *pglA*, glycosyltransferase 18/48
Nm50: *katA*, catalase 60/22
Nm60: probable transmembrane transport protein 4/37', 9/37, 80/37'
Nm65: probable lipoprotein 19/44
Nm67: unknown 49/30
Nm70: *rluC*, probable ribosomal large subunit pseudouridine synthase C 1/44
Nm73: probable amino-acid transport protein 14/46, 17/12
Nm77: *gidB*, probable glucose inhibited division protein B homolog 20/24
Nm83: *dxr*, probable 1-deoxy-D-xylulose-5-phosphate reductoisomerase 80/24
Nm84: probable integral membrane protein 5/38

Nm155: unknown 7/37, 13/31', 25/45'
Nm157: unknown 47/48
Nm160: probable two-component sensor 92/36
Nm162: SUN homolog 19/43
Nm165: probable periplasmic protein 8/7, 8/15, 95/23
Nm173: unknown 51/35
Nm182: probable lipoprotein 9/42
Nm183: *glrS*, sodium/glutamate symport carrier protein 72/40
Nm184: unknown 19/1, 23/8, 57/10
Nm185: *lipB*, capsule polysaccharide modification protein 19/14', 22/14', 25/9, 86/2
Nm186: *lipA*, capsule polysaccharide modification protein 41/29, 80/4, 93/19
Nm193: probable modification methylase 15/20, 25/6
Nm195: *ctrD*, probable capsule polysaccharide export ATP-binding protein 17/5', 18/15', 93/47
Nm198: *ctrA*, capsule polysaccharide export outer membrane protein 13/16, 43/8

Nm207: probable integral membrane protein 55/35
Nm221: possible transposase for IS1106 12/5
Nm225: possible lipoprotein 5/36, 15/9
Nm228: unknown 28/25
Nm229: unknown 93/38
Nm233: probable lipoprotein 16/20
Nm247: *mutS*, DNA mismatch repair protein 11/7, 11/16
Nm251: probable periplasmic protein 1/21, 12/7', 12/17'', 12/19', 19/13'', 94/38
Nm255: *ftsX*, probable ABC transporter integral membrane protein 16/5, 93/43
Nm259: probable transmembrane transport protein 92/11
Nm274: possible glycerate dehydrogenase 39/20', 47/12'
Nm279: probable membrane-bound lytic murein transglycosylase 6/29, 70/13, 76/7, 95/47
Nm285: probable lipoprotein 38/2
Nm287: *thpA*, probable thiamin-binding periplasmic protein 1/38

515 genes mutated on 29/11/01

The underlined mutants present an increased sensitivity to the bactericidal action of the complement of human serum. The figures in bold identify each mutant by pool number/mutant number.

- Nm2: *nuoL*, NADH dehydrogenase I chain L 8/1
 Nm3: unknown 35/25
 Nm10: *nuoG*, NADH dehydrogenase I chain G 16/33, 26/39
 Nm15: *nuoE*, NADH dehydrogenase I chain E 8/41
 Nm17: *nuoC*, NADH dehydrogenase I chain C 29/44, 57/25
 Nm18: *nuoB*, NADH dehydrogenase I chain B 7/39', 64/45'
 Nm20: probable integral membrane protein 20/44
 Nm22: possible transposase for IS1016 9/17
 Nm24: unknown 20/7
 Nm29: unknown 93/8
 Nm37: unknown 95/37
 Nm39: unknown 5/31, 24/16', 53/27', 93/13
 Nm42: *pyrD*, dihydroorotate dehydrogenase 79/39
 Nm47: probable transmembrane transport protein 71/19
 Nm48: *pglA*, glycosyltransferase 18/48
 Nm50: *kata*, catalase 60/22
 Nm60: probable transmembrane transport protein 4/37', 9/37, 80/37'
 Nm65: probable lipoprotein 19/44
 Nm67: unknown 49/30
 Nm70: *rluC*, probable ribosomal large subunit pseudouridine synthase C 1/44
 Nm73: probable amino-acid transport protein 14/46, 17/12
 Nm77: *gidB*, probable glucose inhibited division protein B homolog 20/24
 Nm83: *chr*, probable 1-deoxy-D-xylulose-5-phosphate reductoisomerase 80/24
 Nm84: probable integral membrane protein 5/38

 Nm155: unknown 7/37, 13/31', 25/45'
 Nm157: unknown 47/48
 Nm160: probable two-component sensor 92/36
 Nm162: SUN homolog 19/43
 Nm165: probable periplasmic protein 8/7, 8/15, 95/23
 Nm173: unknown 51/35
 Nm182: probable lipoprotein 9/42
 Nm183: *gltS*, sodium/glutamate symport carrier protein 72/40
 Nm184: unknown 19/1, 23/8, 57/10
 Nm185: *lipB*, capsule polysaccharide modification protein 19/14', 22/14', 25/9, 86/2
 Nm186: *lipA*, capsule polysaccharide modification protein 41/29, 80/4, 93/19
 Nm193: probable modification methylase 15/20, 25/6
 Nm195: *crd*, capsule polysaccharide export ATP-binding protein 17/5', 18/15', 93/47
 Nm198: *cirA*, capsule polysaccharide export outer membrane protein 13/16, 43/8

 Nm207: probable integral membrane protein 55/35
 Nm221: possible transposase for IS106 12/5
 Nm225: possible lipoprotein 5/36, 15/9
 Nm228: unknown 28/25
 Nm229: unknown 93/38
 Nm233: probable lipoprotein 16/20
 Nm247: *mutS*, DNA mismatch repair protein 11/7, 11/16
 Nm251: probable periplasmic protein 1/21, 12/7', 12/17'', 12/19', 19/13'', 94/38
 Nm255: *ftsX*, probable ABC transporter integral membrane protein 16/5, 93/43
 Nm259: probable transmembrane transport protein 92/11
 Nm274: possible glycerate dehydrogenase 39/20', 47/12'
 Nm279: probable membrane-bound lytic murein transglycosylase 6/29, 70/13, 76/7, 95/47
 Nm235: probable lipoprotein 38/2

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Nm289: unknown 16/1
Nm292: unknown 10/43
Nm293: *pilC2*, pilus-associated protein 2/26, 94/28
Nm298: probable symport protein 95/14

Figure 2A
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Nm307: unknown 12/28
Nm319: *mafB'*, possible MafB alternative C-terminus 8/30
Nm320: unknown 13/43
Nm325: *mafA*, adhesin 5/25
Nm348: putative nuclease 3/30, 20/4
Nm349: probable integral membrane protein 46/7
Nm353: probable integral membrane protein 22/45, 90/40
Nm356: possible transferase 55/48
Nm365: probable permease 4/33
Nm368: probable integral membrane protein 12/36
Nm369: *hemK*, HemK protein 81/39
Nm370: probable integral membrane protein 46/43
Nm372: unknown 7/18', 8/27'
Nm374: *ppc*, phosphoenolpyruvate carboxylase 18/33, 18/38, 84/2
Nm380: unknown 46/35
Nm382: unknown 10/9
Nm397: *thiC*, thiamin biosynthesis protein 13/33

Nm409: probable amino-acid transport protein 4/24
Nm413: *gntP*, probable gluconate permease 10/47
Nm414: probable permease 2/16, 5/46
Nm422: probable pseudouridine synthase 6/9', 13/19, 20/15', 77/18
Nm425: unknown 47/7
Nm428: conserved hypothetical protein 3/31
Nm433: *hrpA'*, ATP-dependent DNA helicase 44/4
Nm434: hypothetical inner membrane protein 61/14
Nm436: hypothetical inner membrane protein 93/32
Nm441: conserved hypothetical protein 12/25
Nm445: *purL*, phosphoribosylformylglycinamide synthase 4/17, 10/14', 11/8', 75/34
Nm457: *iga2*, IgA-specific serine endopeptidase 9/21, 40/31
Nm465: hypothetical inner membrane protein 71/2
Nm478: possible outer membrane peptidase 6/43
Nm481: unknown 27/21
Nm485: probable ABC transport ATP-binding subunit 5/4, 16/45
Nm486: possible ABC transport inner-membrane subunit 15/32
Nm489: hypothetical protein 61/13
Nm490: possible periplasmic/outer membrane protein 96/22
Nm497: probable inner membrane protein 71/18
Nm499: *regG*, possible regulator of *pilE* expression 7/44

Nm503: possible transglycosylase 6/19, 11/17, 16/17
Nm506: possible lipoprotein 6/12
Nm512: *atpI*, probable ATP synthase I 8/23
Nm524: *lgtA*, lacto-N-neotetraose biosynthesis glycosyl transferase 3/8, 10/2, 21/21, 45/34
Nm531: pseudogene, probable transposase remnant 90/36
Nm546: unknown 20/9
Nm559: *leuS*, probable leucyl-tRNA synthetase 68/22
Nm560: *drg*, probable type II restriction endonuclease 57/15
Nm580: *argA*, probable acetylglutamate synthase 7/25
Nm582: *pyrE*, probable orotate phosphoribosyltransferase 19/36, 57/31
Nm587: *fba*, probable fructose-1,6-bisphosphate aldolase 21/25, 21/47
Nm592: *hemI*, probable glutamate-1-semialdehyde 2,1-aminomutase 47/10
Nm594: *orn*, probable oligoribonuclease 14/25
Nm599: *queA*, probable S-adenosylmethionine-ribosyltransferase-isomerase 91/2, 96/23

**Figure 2A
(cntd)**

Nm287: *tbpA*, probable thiamin-binding periplasmic protein 1/38
 Nm289: unknown 16/1
 Nm292: unknown 10/43
 Nm293: *pilC2*, pilus-associated protein 2/26, 94/28
 Nm298: probable symport protein 95/14

 Nm307: unknown 12/28
 Nm319: *mafB'*, possible MafB alternative C-terminus 8/30
 Nm320: unknown 13/43
 Nm325: *mafA*, adhesin 5/25
 Nm348: putative nuclease 3/30, 20/4
 Nm349: probable integral membrane protein 46/7
 Nm353: probable integral membrane protein 22/45, 90/40
 Nm356: possible transferase 55/48
 Nm365: probable permease 4/33
 Nm368: probable integral membrane protein 12/36
 Nm369: *hemK*, HemK protein 81/39
 Nm370: probable integral membrane protein 46/43
 Nm372: unknown 7/18', 8/27'
 Nm374: *ppc*, phosphoenolpyruvate carboxylase 18/33, 18/38, 84/2
 Nm380: unknown 46/35
 Nm382: unknown 10/9
 Nm397: *thiC*, thiamin biosynthesis protein 13/33

 Nm409: probable amino-acid transport protein 4/24
 Nm413: *gntP*, probable gluconate permease 10/47
 Nm414: probable permease 2/16, 5/46
 Nm422: probable pseudouridine synthase 6/9', 13/19, 20/15', 77/18
 Nm425: unknown 47/7
 Nm428: conserved hypothetical protein 3/31
 Nm433: *hpaA'*, ATP-dependent DNA helicase 44/4
 Nm434: hypothetical inner membrane protein 61/14
 Nm436: hypothetical inner membrane protein 93/32
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 Nm445: *purL*, phosphoribosylformylglycinamide synthase 4/17, 10/14', 11/8', 75/34
 Nm457: *iga2*, IgA-specific serine endopeptidase 9/21, 40/31
 Nm465: hypothetical inner membrane protein 71/2
 Nm478: possible outer membrane peptidase 6/43
 Nm481: unknown 27/21
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 Nm486: possible ABC transport inner-membrane subunit 15/32
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 Nm506: possible lipoprotein 6/12
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 Nm524: *lgtA*, lacto-N-neotetraose biosynthesis glycosyl transferase 3/8, 10/2, 21/21, 45/34
 Nm531: pseudogene, probable transposase remnant 90/36
 Nm546: unknown 20/9
 Nm559: *leuS*, probable leucyl-tRNA synthetase 68/22
 Nm560: *arg*, probable type II restriction endonuclease 57/15
 Nm580: *argA*, probable acetylglutamate synthase 7/25
 Nm582: *pyrE*, probable orotate phosphoribosyltransferase 19/36, 57/31
 Nm587: *fba*, probable fructose-1,6-bisphosphate aldolase 21/25, 21/47
 Nm592: *hemL*, probable glutamate-1-semialdehyde 2,1-aminomutase 47/10
 Nm594: *orn*, probable oligoribonuclease 14/25
 Nm599: *queA*, probable S-adenosylmethionine-ribosyltransferase-isomerase 91/2, 96/23

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Figure 2A
(cntd)

Nm600: unknown 11/28
 Nm601: probable *lysR*-family transcriptional regulator 47/37
 Nm602: *carB*, carbamoyl phosphate synthase 2/13, 94/39
 Nm613: probable *marR*-family regulator 92/41
 Nm618: hypothetical protein 5/14, 91/41, 92/45
 Nm619: possible lipopolysaccharide modification acyltransferase 31/22, 46/36, 47/14, 96/11
 Nm629: unknown 9/6
 Nm630: unknown 10/4
 Nm631: unknown 6/46, 9/23, 15/22, 34/9
 Nm636: *avtA*, probable valine-pyruvate aminotransferase 7/22
 Nm638: *pglC*, pilin glycosylation protein 68/25
 Nm639: *pglB*, pilin glycosylation protein 90/45, 93/45
 Nm643: possible lipopolysaccharide biosynthesis translocase 43/13
 Nm646: unknown 7/16
 Nm650: *pilQ*, pilus secretin 10/33, 72/13
 Nm654: *pilM*, probable pilus assembly protein 11/33, 19/33
 Nm670: possible two-component system sensor kinase 1/14
 Nm672: unknown 69/23
 Nm679: unknown 1/43, 15/17
 Nm687: probable periplasmic protein 96/46
 Nm688: *fhaB*-like gene 3/24, 14/31, 16/2, 48/7, 87/6
 Nm690: unknown 10/21, 22/11
 Nm691: unknown, Asn-rich N-terminus 46/46
 Nm692: unknown 4/7, 20/27
 Nm693: unknown within a region of low G+C % 3/19
 Nm694: unknown within a region of low G+C % 7/17
 Nm696: unknown 1/40, 7/42

Nm714: probable transmembrane hexose transporter 2/14, 5/47
 Nm715: probable transmembrane transport protein 1/2, 6/45, 15/40
 Nm720: unknown 4/19, 14/7
 Nm722: probable transmembrane transport protein 41/25
 Nm725: *adhA*, probable alcohol dehydrogenase 7/20, 51/22
 Nm726: probable pilin (*acfP*) 11/24
 Nm729: probable ABC transporter ATP-binding protein 92/43
 Nm730: possible thiol-disulphide interchange protein 7/9, 10/18
 Nm740: unknown 6/10
 Nm741: possible ubiquinone biosynthesis protein 92/15
 Nm747: *nqrF*, probable Na⁺-translocating NADH-ubiquinone reductase subunit F 90/34
 Nm750: *nqrC*, probable Na⁺-translocating NADH-ubiquinone reductase subunit C 12/45
 Nm752: *nqrA*, probable Na⁺-translocating NADH-ubiquinone reductase subunit A 19/27, 96/39
 Nm753: possible membrane protein 7/46', 19/19, 28/21', 51/14, 95/45
 Nm755: unknown 70/11', 71/6', 73/5, 73/18
 Nm762: hypothetical protein 18/16, 90/29
 Nm786: possible membrane protein 78/23
 Nm796: unknown 92/2

Nm800: possible integral membrane protein 7/10, 29/28, 52/1, 69/14
 Nm801: unknown 6/5', 12/8'
 Nm802: unknown 30/25
 Nm804: possible sec-independent protein translocase component 93/25
 Nm816: probable polyamine permease ATP-binding protein 19/8
 Nm817: probable polyamine permease inner membrane protein 9/36
 Nm819: possible oxidoreductase 96/31
 Nm820: *amtB*, probable ammonium transporter 5/30
 Nm826: *ppsA*, probable phosphoenolpyruvate synthase 8/47
 Nm827: unknown 7/11
 Nm828: probable phosphatase 36/3
 Nm832: possible glycosyl transferase 14/29, 48/26
 Nm843: *fhpB*, probable iron-uptake permease inner membrane protein 56/34

Nm600: unknown 11/28
 Nm601: probable *lysR*-family transcriptional regulator 47/37
 Nm602: *carB*, carbamoyl phosphate synthase 2/13, 94/39
 Nm613: probable *marR*-family regulator 92/41
 Nm618: hypothetical protein 5/14, 91/41, 92/45
 Nm619: possible lipopolysaccharide modification acyltransferase 31/22, 46/36, 47/14, 96/11
 Nm629: unknown 9/6
 Nm630: unknown 10/4
 Nm631: unknown 6/46, 9/23, 15/22, 34/9
 Nm636: *avtA*, probable valine-pyruvate aminotransferase 7/22
 Nm638: *pglC*, pilin glycosylation protein 68/25
 Nm639: *pglB*, pilin glycosylation protein 90/45, 93/45
 Nm643: possible lipopolysaccharide biosynthesis translocase 43/13
 Nm646: unknown 7/16
 Nm650: *pilQ*, pilus secretin 10/33, 72/13
 Nm654: *pilM*, probable pilus assembly protein 11/33, 19/33
 Nm670: possible two-component system sensor kinase 1/14
 Nm672: unknown 69/23
 Nm679: unknown 1/43, 15/17
 Nm687: probable periplasmic protein 96/46
 Nm688: *fhaB*-like gene 3/24, 14/31, 16/2, 48/7, 87/6
 Nm690: unknown 10/21, 22/11
 Nm691: unknown, Asn-rich N-terminus 46/46
 Nm692: unknown 4/7, 20/27
 Nm693: unknown within a region of low G+C % 3/19
 Nm694: unknown within a region of low G+C % 7/17
 Nm696: unknown 1/40, 7/42

 Nm714: probable transmembrane hexose transporter 2/14, 5/47
 Nm715: probable transmembrane transport protein 1/2, 6/45, 15/40
 Nm720: unknown 4/19, 14/7
 Nm722: probable transmembrane transport protein 41/25
 Nm725: *adhA*, probable alcohol dehydrogenase 7/20, 51/22
 Nm726: probable pilin (*acP*) 11/24
 Nm729: probable ABC transporter ATP-binding protein 92/43
 Nm730: possible thiol-disulphide interchange protein 7/9, 10/18
 Nm740: unknown 6/10
 Nm741: possible ubiquinone biosynthesis protein 92/15
 Nm747: *nqrF*, probable Na⁺-translocating NADH-ubiquinone reductase subunit F 90/34
 Nm750: *nqrC*, probable Na⁺-translocating NADH-ubiquinone reductase subunit C 12/45
 Nm752: *nqrA*, probable Na⁺-translocating NADH-ubiquinone reductase subunit A 19/27, 96/39
 Nm753: possible membrane protein 7/46', 19/19, 28/21', 51/14, 95/45
 Nm755: unknown 70/11', 71/6', 73/5, 73/18
 Nm762: hypothetical protein 18/16, 90/29
 Nm786: possible membrane protein 78/23
 Nm796: unknown 92/2

 Nm800: possible integral membrane protein 7/10, 29/28, 52/1, 69/14
 Nm801: unknown 6/5', 12/8'
 Nm802: unknown 30/25
 Nm804: possible sec-independent protein translocase component 93/25
 Nm816: probable polyamine permease ATP-binding protein 19/8
 Nm817: probable polyamine permease inner membrane protein 9/36
 Nm819: possible oxidoreductase 96/31
 Nm820: *amtB*, probable ammonium transporter 5/30
 Nm826: *ppsA*, probable phosphoenolpyruvate synthase 8/47
 Nm827: unknown 7/11
 Nm828: probable phosphatase 36/3
 Nm832: possible glycosyl transferase 14/29, 48/26

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Figure 2A
(cntd)

Nm845: unknown 6/8
 Nm847: *argH*, probable argininosuccinate lyase 95/5
 Nm848: *galU*, probable UTP-glucose-1-phosphate uridylyltransferase 32/37
 Nm867: *ampD*, probable anhydro-N-acetylmuramyl-tripeptide amidase 48/6
 Nm868: possible periplasmic protein 46/19
 Nm873: possible periplasmic protein 11/5
 Nm879: *trpA*, probable tryptophan synthase α chain 19/24, 65/48
 Nm884: *pyrC*, probable dihydroorotase 1/37, 89/9
 Nm888: *rnc*, probable ribonuclease III 6/47
 Nm890: *trpF*, probable N-(5'-phosphoribosyl)anthranilate isomerase 95/39
 Nm892: *purF*, probable amidophosphoribosyltransferase 60/4

 Nm904: *trpB*, probable tryptophan synthase β chain 5/41, 8/40, 27/34', 85/25'
 Nm905: *iga*, IgA1 protease 1/39, 7/1, 9/25, 12/34
 Nm909: probable transmembrane transport protein 1/28, 9/22
 Nm915: unknown 3/37
 Nm928: *tgt*, probable queuine tRNA-ribosyltransferase 95/9
 Nm935: unknown 4/28, 75/44
 Nm941: unknown 2/45
 Nm942: *bioA*, probable adenosylmethionine-8-amino-7-oxononanoate aminotransferase 6/6, 33/2
 Nm944: unknown 7/13
 Nm948: unknown 32/26
 Nm952: *recN*, probable DNA repair protein 68/11
 Nm955: unknown 5/7
 Nm962: probable D-alanyl-D-alanine-endopeptidase 1/48, 56/18, 96/16
 Nm968: *purC*, probable phosphoribosylaminoimidazole-succinocarboxamide synthase 5/15
 Nm973: probable integral membrane protein 7/40, 44/34
 Nm977: *lepA*, probable GTP-binding protein 90/15
 Nm979: *pilT2*, possible pilus retraction protein 90/19
 Nm981: possible pilus biogenesis protein 11/22
 Nm982: unknown 1/24, 7/33
 Nm987: probable secreted protein 64/5
 Nm990: unknown 80/2
 Nm993: possible periplasmic protein 72/33
 Nm994: possible periplasmic protein 16/39
 Nm995: *recB*, probable exodeoxyribonuclease V β chain 8/42, 9/28, 41/35
 Nm999: probable amino acid permease integral membrane protein 73/39

 Nm1001: *pgm*, phosphoglucomutase 2/46, 6/35, 25/5, 94/2
 Nm1002: *ppiB*, probable peptidyl-prolyl cis-trans isomerase B 94/18
 Nm1003: probable transmembrane transport protein 29/42
 Nm1008: *ftsI*, probable cell division protein 15/1
 Nm1012: probable carbon-sulphur lyase 6/28, 92/4
 Nm1015: probable NAD(P)H-flavin oxidoreductase 25/14, 29/32
 Nm1016: probable RNA-binding protein 93/44
 Nm1020: probable *tetR*-family transcriptional regulator 28/41
 Nm1022: possible transmembrane efflux protein 8/22, 37/27
 Nm1034: *rfaE*, probable ADP-heptose synthetase 13/6
 Nm1035: *nmgII*, probable modification methylase 60/25, 93/11
 Nm1037: *rfaL*, probable ADP-L-glycero-mannoheptose epimerase 7/30, 47/39
 Nm1048: unknown 18/3, 35/37
 Nm1052: *recJ*, probable single-stranded-DNA-specific exonuclease 43/9
 Nm1054: possible periplasmic protein 6/2
 Nm1056: unknown 5/1
 Nm1062: *rdgC*, unknown 2/39
 Nm1073: unknown 11/13, 83/7
 Nm1074: possible membrane protein 10/16, 47/27
 Nm1084: possible periplasmic protein 15/26
 Nm1086: unknown 7/35
 Nm1087: possible transferase 4/29, 84/17
 Nm1090: possible periplasmic protein 7/27, 19/12
 Nm1107: possible membrane protein 96/8
 Nm1108: possible membrane protein 34/7
 Nm1110: probable pilin 12/39, 41/23
 Nm1111: unknown 18/19
 Nm1118: *lx*, CMP-N-acetylmuramyl- β -galactoside- α -2,3-sialyltransferase 9/46, 65/40, 73/46, 94/8
 Nm1126: probable transmembrane transport protein 46/38
 Nm1136: *metX*, probable homoserine O-acetyltransferase 3/11, 14/42
 Nm1138: *rpmE2*, possible additional 50S ribosomal protein L31 96/2
 Nm1139: *metH*, probable 5,10-methylenetetrahydrofolate reductase 92/29
 Nm1140: *metE*, probable 5-methyltetrahydropteroylglutamate-homocysteine methyltransferase 71/7

Nm843: *fbpB*, probable iron-uptake permease inner membrane protein 56/34
 Nm845: unknown 6/8
 Nm847: *argH*, probable argininosuccinate lyase 95/5
 Nm848: *galII*, probable UTP-glucose-1-phosphate uridylyltransferase 32/37
 Nm867: *ampD*, probable anhydro-N-acetylmuramyl-tripeptide amidase 48/6
 Nm868: possible periplasmic protein 46/19
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 Nm884: *pyrC*, probable dihydroorotase 1/37, 89/9
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 Nm890: *trpF*, probable N-(5'-phosphoribosyl)anthranilate isomerase 95/39
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 Nm928: *tgt*, probable queuine tRNA-ribosyltransferase 95/9
 Nm935: unknown 4/28, 75/44
 Nm941: unknown 2/45
 Nm942: *bioA*, probable adenosylmethionine-8-amino-7-oxononanoate aminotransferase 6/6, 33/2
 Nm944: unknown 7/13
 Nm948: unknown 32/26
 Nm952: *recN*, probable DNA repair protein 68/11
 Nm955: unknown 5/7
 Nm962: probable D-alanyl-D-alanine-endopeptidase 1/48, 56/18, 96/16
 Nm968: *purC*, probable phosphoribosylaminoimidazole-succinocarboxamide synthase 5/15
 Nm973: probable integral membrane protein 7/40, 44/34
 Nm977: *lepA*, probable GTP-binding protein 90/15
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 Nm1086: unknown 7/35Nm1087: possible transferase 4/29, 84/17
 Nm1090: possible periplasmic protein 7/27, 19/12
 Nm1107: possible membrane protein 96/8Nm1108: possible membrane protein 34/7
 Nm1110: probable pilin 12/39, 41/23

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Nm1143: *sdhC*, probable succinate dehydrogenase cytochrome B subunit 92/23Nm1145: *sdhA*, probable succinate dehydrogenase flavoprotein subunit 4/39Nm1146: *sdhB*, probable succinate dehydrogenase iron-sulphur protein 18/44

Nm1148: *gluA*, probable citrate synthase 16/6', 20/34', 81/36Nm1149: *sucA*, probable 2-oxoglutarate dehydrogenase E1 component 15/24Nm1152: possible membrane protein 13/7, 93/18, 95/6Nm1162: unknown 96/1

Nm1163: *trpG*, probable anthranilate synthase component II 26/22', 48/1'Nm1164: *trpD*, probable anthranilate phosphoribosyltransferase 9/19Nm1174: unknown 11/45Nm1184: possible lipoprotein 11/25Nm1186: unknown 12/18Nm1195: unknown

6/33 Nm1200:

probable surface fibril protein 47/19', 52/12'Nm1206: probable oxidoreductase 6/48, 34/8, 77/17Nm1207: unknown 14/24Nm1228: unknown within a region of unusually low G+C % 23/29Nm1243: probable sulphate-binding protein 7/26Nm1248: possible periplasmic protein 5/37Nm1249: *abcZ*, probable ABC transporter ATP-binding protein 2/8, 78/6Nm1250: *dedA*, hypothetical protein 19/5Nm1254: *glyA*, probable serine hydroxymethyltransferase 42/20Nm1255: *ggt*, probable gamma-glutamyltranspeptidase 14/8, 92/27, 94/15Nm1263: unknown 89/16Nm1272: unknown 95/2

Nm1276: possible membrane protein 5/43, 16/13, 20/40Nm1285: unknown 94/37

Nm1286: possible phage transposase
82/19 Nm1307:

unknown 95/32

Nm1313: unknown 18/13, 22/18, 94/35Nm1315: unknown 18/31, 93/10

Nm1325: possible phage tail fibre protein 15/19Nm1331: ABC transporter ATP-binding protein 3/43, 22/25

Nm1334: possible periplasmic protein 1/32, 43/17

Nm1341: unknown 12/46

Nm1348: unknown 76/13

Nm1351: possible RNA methyltransferase 76/37

Nm1356: *mpl*, possible UDP-N-acetylmuramate-L-alanyl-L-D-glutamyl-meso-diaminopimelate ligase 11/38, 12/15

Nm1362: *cysI*, probable sulphite reductase β subunit 25/23

Nm1363: *cysJ*, probable sulphite reductase α subunit 4/38, 11/12

Nm1365: *cysD*, probable sulphate adenylate transferase subunit 2 19/29

Nm1366: *cysH*, probable phosphoadenosinephosphosulfate reductase 8/32

Nm1367: *cysG*, sirohaem synthase 53/16

Nm1369: unknown, similar to the C-terminal half of bacterial hypothetical proteins 8/34, 63/5

Nm1371: *vacB*, probable ribonuclease 40/33

Nm1372: *guaB*, probable inosine-5'-monophosphate dehydrogenase 65/17

Nm1373: unknown 11/32, 27/42

Nm1375: possible transcriptional regulator 95/8

Nm1381: probable integral membrane protein 74/27

Nm1385: probable type I restriction-modification system modification protein 93/14

Nm1393: possible ABC transporter ATP-binding protein 11/31

Nm1395: *hom*, probable homoserine dehydrogenase 16/37

Nm1401: *recD*, exodeoxyribonuclease V α subunit 13/5', 14/39', 31/25

Nm1408: unknown 12/31

Nm1409: probable ABC-transporter ATP-binding protein 10/42, 18/21

Nm1415: unknown 7/47

Nm1417: possible molybdopterin-guanine dinucleotide biosynthesis protein A 10/20, 34/28

Nm1418: probable two-component system sensor kinase 87/16

Nm1421: *purM*, probable phosphoribosylformylglycinamide cyclo-ligase 7/5

Nm1425: *ribA*, probable GTP cyclohydrolase II 91/3

Nm1427: probable glycosyl transferase 42/9

Nm1435: unknown within a region of low G+C % 19/6, 90/47

Nm1438: possible integral membrane protein 15/6

Nm1440: *thrC*, probable threonine synthase 87/24

Nm1441: unknown 21/31

Nm1445: unknown 9/15

Nm1448: *radC*, probable DNA repair protein 3/36, 4/45

Nm1450: *leuC*, probable 3-isopropylmalate dehydratase large subunit 68/2

Nm1456: *leuB*, probable 3-isopropylmalate dehydrogenase 4/9, 40/35

Nm1459: *aspA*, probable aspartate ammonia-lyase 19/34, 44/45, 52/9

Nm1111: unknown 18/19
 Nm1118: *lyt*, CMP-N-acetylmuramic- β -galactoside C-2,3-sialyltransferase 9/46, 65/40, 73/46, 94/8
 Nm1126: probable transmembrane transport protein 46/38
 Nm1136: *metX*, probable homoserine O-acetyltransferase 3/11, 14/42
 Nm1138: *rpmE2*, possible additional 50S ribosomal protein L31 96/2
 Nm1139: *metF*, probable 5,10-methylenetetrahydrofolate reductase 92/29
 Nm1140: *metF*, probable 5-methyltetrahydropteroylglutamate-homocysteine methyltransferase 71/7
 Nm1143: *sdhC*, probable succinate dehydrogenase cytochrome B subunit 92/23
 Nm1145: *sdhA*, probable succinate dehydrogenase flavoprotein subunit 4/39
 Nm1146: *sdhB*, probable succinate dehydrogenase iron-sulphur protein 18/44
 Nm1148: *glcA*, probable citrate synthase 16/6', 20/34', 81/36
 Nm1149: *sucA*, probable 2-oxoglutarate dehydrogenase E1 component 15/24
 Nm1152: possible membrane protein 13/7, 93/18, 95/6
 Nm1162: unknown 96/1
 Nm1163: *trpG*, probable anthranilate synthase component II 26/22', 48/1'
 Nm1164: *trpD*, probable anthranilate phosphoribosyltransferase 9/19
 Nm1174: unknown 11/45
 Nm1184: possible lipoprotein 11/25
 Nm1186: unknown 12/18
 Nm1195: unknown 6/33

 Nm1200: probable surface fibril protein 47/19', 52/12'
 Nm1206: probable oxidoreductase 6/48, 34/8, 77/17
 Nm1207: unknown 14/24
 Nm1228: unknown within a region of unusually low G+C % 23/29
 Nm1243: probable sulphate-binding protein 7/26
 Nm1248: possible periplasmic protein 5/37
 Nm1249: *abcZ*, probable ABC transporter ATP-binding protein 2/8, 78/6
 Nm1250: *dedA*, hypothetical protein 19/5
 Nm1254: *glyA*, probable serine hydroxymethyltransferase 42/20
 Nm1255: *ggt*, probable gamma-glutamyltranspeptidase 14/8, 92/27, 94/15
 Nm1263: unknown 89/16
 Nm1272: unknown 95/2
 Nm1276: possible membrane protein 5/43, 16/13, 20/4
 Nm1285: unknown 94/37
 Nm1286: possible phage transposase 82/19

 Nm1307: unknown 95/32
 Nm1313: unknown 18/13, 22/18, 94/35
 Nm1315: unknown 18/31, 93/10
 Nm1325: possible phage tail fibre protein 15/19
 Nm1331: ABC transporter ATP-binding protein 3/43, 22/25
 Nm1334: possible periplasmic protein 1/32, 43/17
 Nm1341: unknown 12/46
 Nm1348: unknown 76/13
 Nm1351: possible RNA methyltransferase 76/37
 Nm1356: *npx*, possible UDP-N-acetylmuramate-L-alanyl-D-glutamyl-meso-diaminopimelate lyase 11/58, 12/15
 Nm1362: *cysI*, probable sulphite reductase β subunit 25/23
 Nm1363: *cysI*, probable sulphite reductase α subunit 4/38, 11/12
 Nm1365: *cysD*, probable sulphate adenylate transferase subunit 2 19/29
 Nm1366: *cysH*, probable phosphoadenosinephosphosulfate reductase 8/32
 Nm1367: *cysG*, sirohaem synthase 53/16
 Nm1369: unknown, similar to the C-terminal half of bacterial hypothetical proteins 8/34, 63/5
 Nm1371: *vacB*, probable ribonuclease 40/33
 Nm1372: *guaB*, probable inosine-5'-monophosphate dehydrogenase 65/17
 Nm1373: unknown 11/32, 27/42
 Nm1375: possible transcriptional regulator 95/8
 Nm1381: probable integral membrane protein 74/27
 Nm1385: probable type I restriction-modification system modification protein 93/14
 Nm1393: possible ABC transporter ATP-binding protein 11/31
 Nm1395: *hom*, probable homoserine dehydrogenase 16/37

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**Figure 2A
(cntd)**

Nm1460: probable integral membrane protein 11/27
 Nm1461: probable *dnaJ*-family protein 5/35
 Nm1465: unknown 95/25
 Nm1466: probable type III restriction-modification system endonuclease protein 8/43
 Nm1467: type III restriction-modification system 4/25
 Nm1473: unknown 15/35
 Nm1475: unknown 7/31, 8/8', 8/18', 92/5'', 92/12'', 92/44
 Nm1482: probable acyl-CoA ligase 5/39
 Nm1483: probable transmembrane transport protein 10/34, 14/11
 Nm1485: *gcr*, site-specific recombinase 13/39, 15/48
 Nm1491: *mfd*, transcription-repair coupling factor 14/3

Nm1500: probable modification methylase 19/37', 36/37'
 Nm1507: possible membrane-bound lytic murein transglycosylase 5/28, 86/5, 90/27
 Nm1508: possible ribosomal small subunit pseudouridine synthase 19/21, 56/44
 Nm1509: possible sodium-dependent transporter 25/25
 Nm1518: *adhC*, alcohol dehydrogenase class-III, glutathione-dependent formaldehyde dehydrogenase 18/25, 34/26, 94/48
 Nm1519: *esd*, esterase D 13/44
 Nm1523: possible lipoprotein 19/4
 Nm1528: *uraA*, uracil permease 10/22, 40/6
 Nm1533: conserved hypothetical integral membrane protein 7/14
 Nm1540: *uvrC*, excinuclease ABC subunit C 63/12
 Nm1541: unknown 3/5
 Nm1542: conserved hypothetical protein 96/42
 Nm1545: *uvrB*, excinuclease ABC subunit B 43/4
 Nm1547: possible secreted lysine-rich protein 8/3
 Nm1557: unknown 11/11
 Nm1558: possible TonB-dependent receptor protein 1/31
 Nm1565: probable aldehyde dehydrogenase 2/36
 Nm1571: iron/sulphur-binding oxidoreductase 90/18
 Nm1574: possible integral membrane transporter 11/35, 46/17, 74/48
 Nm1575: *xseA*, exonuclease VII large subunit 6/23
 Nm1577: unknown 12/6
 Nm1579: unknown 19/48, 66/14
 Nm1580: probable ATP-dependent RNA helicase 53/9
 Nm1584: *argD*, acetylornithine aminotransferase 9/48
 Nm1589: conserved hypothetical protein 45/18
 Nm1590: probable type III restriction/modification system modification methylase 15/5
 Nm1592: *lldA*, L-lactate dehydrogenase 8/4', 20/1', 77/12

Nm1603: unknown 96/13
 Nm1617: *sodC*, superoxide dismutase 1/47
 Nm1639: probable integral membrane protein 61/48
 Nm1642: *porA*, porin, class I outer membrane protein 6/4
 Nm1645: possible lipoprotein 92/13
 Nm1646: phospholipase D-family protein 8/36, 14/4, 40/22, 95/48
 Nm1647: probable integral membrane protein 4/14, 10/3, 27/35
 Nm1660: *rep*, ATP-dependent DNA helicase 22/2
 Nm1665: possible DNA polymerase III subunit 3/48, 9/27
 Nm1679: *ppx/gppA*, possible exophosphatase 4/44
 Nm1687: probable glutamate dehydrogenase 15/36
 Nm1689: possible regulatory protein 9/9
 Nm1690: unknown 11/4

Nm1702: *rbh*, ribonuclease 6/34', 8/39'
 Nm1709: binding-protein-dependent transport systems inner membrane protein 3/28, 8/9
 Nm1715: possible integral membrane protein 11/20
 Nm1720: unknown 8/26
 Nm1722: possible cis-trans isomerase 3/47
 Nm1723: possible proline-rich repeat protein 96/24

Figure 2A
(cntd)

Nm1401: *recD*, exodeoxyribonuclease V α subunit 13/5', 14/39', 31/25
Nm1408: unknown 12/31
Nm1409: probable ABC-transporter ATP-binding protein 10/42, 18/21
Nm1415: unknown 7/47
Nm1417: possible molybdopterin-guanine dinucleotide biosynthesis protein A 10/20, 34/28
Nm1418: probable two-component system sensor kinase 87/16
Nm1421: *purM*, probable phosphoribosylformylglycinamide cyclo-ligase 7/5
Nm1425: *ribA*, probable GTP cyclohydrolase II 91/3
Nm1427: probable glycosyl transferase 42/9
Nm1435: unknown within a region of low G+C % 19/6, 90/47
Nm1438: possible integral membrane protein 15/6
Nm1440: *thrC*, probable threonine synthase 87/24
Nm1441: unknown 21/31
Nm1445: unknown 9/15
Nm1448: *radC*, probable DNA repair protein 3/36, 4/45
Nm1450: *leuC*, probable 3-isopropylmalate dehydratase large subunit 68/2
Nm1456: *leuB*, probable 3-isopropylmalate dehydrogenase 4/9, 40/35
Nm1459: *aspA*, probable aspartate ammonia-lyase 19/34, 44/45, 52/9
Nm1460: probable integral membrane protein 11/27
Nm1461: probable *dnaJ*-family protein 5/35
Nm1465: unknown 95/25
Nm1466: probable type III restriction-modification system endonuclease protein 8/43
Nm1467: type III restriction-modification system 4/25
Nm1473: unknown 15/35
Nm1475: unknown 7/31, 8/8', 8/18', 92/5'', 92/12'', 92/44
Nm1482: probable acyl-CoA ligase 5/39
Nm1483: probable transmembrane transport protein 10/34, 14/11
Nm1485: *gcr*, site-specific recombinase 13/39, 15/48
Nm1491: *mfd*, transcription-repair coupling factor 14/3

Nm1500: probable modification methylase 19/37', 36/37'
Nm1507: possible membrane-bound lytic murein transglycosylase 5/28, 86/5, 90/27
Nm1508: possible ribosomal small subunit pseudouridine synthase 19/21, 56/44
Nm1509: possible sodium-dependent transporter 25/25
Nm1518: *adhC*, alcohol dehydrogenase class III, glutathione-dependent formaldehyde dehydrogenase 18/25, 34/26, 94/48
Nm1519: *esd*, esterase D 13/44
Nm1523: possible lipoprotein 19/4
Nm1528: *uraA*, uracil permease 10/22, 40/6
Nm1533: conserved hypothetical integral membrane protein 7/14
Nm1540: *uvrC*, excinuclease ABC subunit C 63/12
Nm1541: unknown 3/5
Nm1542: conserved hypothetical protein 96/42
Nm1545: *uvrB*, excinuclease ABC subunit B 43/4
Nm1547: possible secreted lysine-rich protein 8/3
Nm1557: unknown 11/11
Nm1558: possible TonB-dependent receptor protein 1/31
Nm1565: probable aldehyde dehydrogenase 2/36
Nm1571: iron/sulphur-binding oxidoreductase 90/18
Nm1574: possible integral membrane transporter 11/35, 46/17, 74/48
Nm1575: *xseA*, exonuclease VII large subunit 6/23
Nm1577: unknown 12/6
Nm1579: unknown 19/48, 66/14
Nm1580: probable ATP-dependent RNA helicase 53/9
Nm1584: *argD*, acetylornithine aminotransferase 9/48
Nm1589: conserved hypothetical protein 45/18
Nm1590: probable type III restriction/modification system modification methylase 15/5
Nm1592: *lldA*, L-lactate dehydrogenase 8/4', 20/1', 77/12

Nm1603: unknown 96/13

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**Figure 2A
(cntd)**

Nm1727: *rfaF*, ADP-heptose:LPS heptosyltransferase II 70/7
 Nm1731: conserved hypothetical protein 94/27
 Nm1740: *lbpB*, lactoferrin-binding protein 37/17
 Nm1751: possible *gntR*-family transcriptional regulator 90/30
 Nm1754: unknown 14/35
 Nm1755: *purN*, phosphoribosylglycinamide transformylase 2/2
 Nm1756: possible peptidyl-prolyl isomerase 1/42, 15/10
 Nm1765: *ilvH*, acetolactate synthase isozyme III small subunit 52/29
 Nm1767: possible lipoprotein 96/34
 Nm1771: *hisC*, histidinol-phosphate aminotransferase 19/39
 Nm1775: partial ORF 93/46
 Nm1778: possible secreted protease 35/1
 Nm1783: AraC-family transcriptional regulator 51/3
 Nm1785: conserved hypothetical integral membrane protein 96/15
 Nm1786: possible polyamine permease substrate-binding protein 29/6, 96/5

Nm1812: *fumA*, fumarate hydratase 2/15, 4/41
 Nm1816: conserved, possible DNA-binding, hypothetical protein 93/12
 Nm1819: conserved hypothetical protein 12/35, 92/21
 Nm1820: *gpxA*, glutathione peroxidase 1/13
 Nm1886: *nor*, nitric oxide reductase 4/30, 8/38, 10/7, 12/43, 13/20, 67/32, 80/16
 Nm1887: *aniA*, nitrite reductase 17/6
 Nm1892: conserved hypothetical protein 2/27
 Nm1894: *serC*, phosphoserine aminotransferase 36/4

Nm1900: possible haemolysin 8/12
 Nm1901: possible sodium-alanine symporter 2/9, 22/5
 Nm1920: *apt*, adenine phosphoribosyltransferase 9/35, 13/35, 34/1, 49/6
 Nm1921: conserved hypothetical protein 58/4, 86/44
 Nm1925: *hmbR*, haemoglobin receptor 11/19, 25/40, 62/9
 Nm1928: hypothetical integral membrane protein 93/33
 Nm1929: hypothetical integral membrane protein 9/40
 Nm1934: *gcvP*, glycine dehydrogenase 4/23, 18/39, 21/35, 32/27, 47/4
 Nm1935: unknown 59/44, 95/10
 Nm1936: probable cytochrome 71/35
 Nm1937: *tyrB*, aromatic amino acid aminotransferase 2/30, 20/19, 47/36, 57/6, 63/23
 Nm1938: *trmA*, tRNA (uracil-5-)-methyltransferase 16/21
 Nm1939: *aroC*, chorismate synthase 88/14
 Nm1940: unknown 23/31, 94/19
 Nm1944: *ldhA*, D-lactate dehydrogenase 60/10
 Nm1946: conserved hypothetical protein 18/28
 Nm1951: unknown 4/6, 37/39
 Nm1953: unknown 80/23
 Nm1957: *fabF*², 3-oxoacyl-(acyl-carrier-protein) synthase II 11/44, 17/8
 Nm1958: *lgtF*, β -1,4-glucosyltransferase 3/15', 23/19', 57/11'', 71/8'', 71/10''
 Nm1960: unknown 2/11
 Nm1961: probable integral membrane ion transporter 10/12
 Nm1969: *mrD*, probable drug efflux protein 36/36
 Nm1970: *mrC*¹, membrane fusion protein 76/30, 92/42
 Nm1973: hypothetical integral membrane protein 2/40, 12/2
 Nm1975: possible integral membrane protein 27/20, 94/9
 Nm1983: *exbD*, biopolymer transport protein 85/3
 Nm1984: *exbB*, biopolymer transport protein 37/33
 Nm1996: *natD*¹, possible periplasmic type I secretion system protein, N-terminal region 6/42

Nm2007: unknown 12/24
 Nm2009: unknown 3/10
 Nm2010: hypothetical protein 5/10, 49/17
 Nm2011: conserved hypothetical protein 94/36, 95/36
 Nm2012: conserved hypothetical protein 43/12

Figure 2A
(cntd)

Nm1617: *sodC*, superoxide dismutase 1/47
 Nm1639: probable integral membrane protein 61/48
 Nm1642: *porA*, porin, class I outer membrane protein 6/4
 Nm1645: possible lipoprotein 92/13
 Nm1646: phospholipase D-family protein 8/36, 14/4, 40/22, 95/48
 Nm1647: probable integral membrane protein 4/14, 10/3, 27/35
 Nm1660: *rep*, ATP-dependent DNA helicase 22/2
 Nm1665: possible DNA polymerase III subunit 3/48, 9/27
 Nm1679: *ppX/gppA*, possible exophosphatase 4/44
 Nm1687: probable glutamate dehydrogenase 15/36
 Nm1689: possible regulatory protein 9/9
 Nm1690: unknown 11/4

 Nm1702: *rbh*, ribonuclease 6/34', 8/39'
 Nm1709: binding-protein-dependent transport systems inner membrane protein 3/28, 8/9
 Nm1715: possible integral membrane protein 11/20
 Nm1720: unknown 8/26
 Nm1722: possible cis-trans isomerase 3/47
 Nm1723: possible proline-rich repeat protein 96/24
 Nm1727: *rfaF*, ADP-heptose:LPS heptosyltransferase II 70/7
 Nm1731: conserved hypothetical protein 94/27
 Nm1740: *lbpB*, lactoferrin-binding protein 37/17
 Nm1751: possible *gntR*-family transcriptional regulator 90/30
 Nm1754: unknown 14/35
 Nm1755: *purN*, phosphoribosylglycinamide transformylase 2/2
 Nm1756: possible peptidyl-prolyl isomerase 1/42, 15/10
 Nm1765: *ilvH*, acetolactate synthase isozyme III small subunit 52/29
 Nm1767: possible lipoprotein 96/34
 Nm1771: *hisC*, histidinol-phosphate aminotransferase 19/39
 Nm1775: partial ORF 93/46
 Nm1778: possible secreted protease 35/1
 Nm1783: AraC-family transcriptional regulator 51/3
 Nm1785: conserved hypothetical integral membrane protein 96/15
 Nm1786: possible polyamine permease substrate-binding protein 29/6, 96/5

 Nm1812: *fumA*, fumarate hydratase 2/15, 4/41
 Nm1816: conserved, possible DNA-binding, hypothetical protein 93/12
 Nm1819: conserved hypothetical protein 12/35, 92/21
 Nm1820: *gpxA*, glutathione peroxidase 1/13
 Nm1886: *nor*, nitric oxide reductase 4/30, 8/38, 10/7, 12/43, 13/20, 67/32, 80/16
 Nm1887: *aniA*, nitrite reductase 17/6
 Nm1892: conserved hypothetical protein 2/27
 Nm1894: *serC*, phosphoserine aminotransferase 36/4

 Nm1900: possible haemolysin 8/12
 Nm1901: possible sodium-alanine symporter 2/9, 22/5
 Nm1920: *apt*, adenine phosphoribosyltransferase 9/35, 13/35, 34/1, 49/6
 Nm1921: conserved hypothetical protein 58/4, 86/44
 Nm1925: *hmbR*, haemoglobin receptor 11/19, 25/40, 62/9
 Nm1928: hypothetical integral membrane protein 93/33
 Nm1929: hypothetical integral membrane protein 9/40
 Nm1934: *gcvP*, glycine dehydrogenase 4/23, 18/39, 21/35, 32/27, 47/4
 Nm1935: unknown 59/44, 95/10
 Nm1936: probable cytochrome 71/35
 Nm1937: *tyrB*, aromatic amino acid aminotransferase 2/30, 20/19, 47/36, 57/6, 63/23
 Nm1938: *trmA*, tRNA (uracil-5-)-methyltransferase 16/21
 Nm1939: *aroC*, chorismate synthase 88/14
 Nm1940: unknown 23/31, 94/19
 Nm1944: *ldhA*, D-lactate dehydrogenase 60/10
 Nm1946: conserved hypothetical protein 18/28

Figure 2A
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Nm2016: *speB*, agmatinase 1/46', 42/46'
 Nm2020: possible integral membrane protein 92/18
 Nm2021: possible phospholipase 3/38
 Nm2028: *amiC*, N-acetylmuramoyl-L-alanine amidase 78/47
 Nm2029: unknown 7/21
 Nm2036: unknown within a region of low G+C % 56/23
 Nm2038: *recO*, DNA repair protein 16/44
 Nm2040: possible integral membrane efflux protein 95/33
 Nm2046: hypothetical integral membrane protein 11/18
 Nm2048: conserved hypothetical protein 41/12, 81/22
 Nm2052: *acnA*, aconitate hydratase 38/25
 Nm2054: *prpC*, citrate synthase 2 8/28, 91/29, 96/30
 Nm2069: probable integral membrane protein 3/4, 31/5
 Nm2076: conserved hypothetical protein 13/2
 Nm2078: possible thiol-disulphide interchange protein 2/31, 24/13
 Nm2083: *putP*, sodium/proline symporter 30/33
 Nm2084: *putA*, bifunctional PutA protein 13/42, 16/10
 Nm2086: *xthA*, exodeoxyribonuclease III 86/31
 Nm2092: *nadB*, L-aspartate oxidase 2/4, 47/24
 Nm2098: *mapA*, possible maltose phosphorylase 5/34
 Nm2099: *galM*, aldose 1-epimerase (mutarotase) 11/10

Nm2100: possible maltose/H⁺ symporter 9/38, 70/40
 Nm2101: ABC transporter ATP-binding protein 1/19', 5/18', 14/4, 38/23, 90/44
 Nm2113: *mafB2*, adhesin 2/7, 4/42, 10/32, 38/24
 Nm2118: hypothetical protein within a region of low G+C % 12/32, 24/11, 68/23
 Nm2120: hypothetical protein within a region of low G+C % 3/23, 78/24
 Nm2122: hypothetical protein within a region of low G+C % 20/13, 29/3
 Nm2123: *frpC'*, possible partial CDS 16/30
 Nm2124: possible outer membrane protein 43/5
 Nm2129: *aroE*, shikimate dehydrogenase 49/7
 Nm2130: *mtgA*, monofunctional biosynthetic peptidoglycan transglycosylase 52/6
 Nm2131: possible ABC transporter ATP-binding protein 13/10
 Nm2136: *tal*, transaldolase 92/9
 Nm2137: hypothetical protein within a region of low G+C % 11/14', 11/42', 96/47
 Nm2140: conserved hypothetical protein 1/11, 4/13, 66/4
 Nm2142: possible periplasmic hypothetical protein 46/40
 Nm2145: possible morphogene 19/45, 23/18, 32/22, 75/47
 Nm2146: *tspA*, *Neisseria*-specific antigen protein 9/9
 Nm2151: *ilvE*, probable branched-chain amino acid aminotransferase 41/31, 66/34
 Nm2155: *pilG*, pilus-assembly protein 2/19, 14/45, 25/19, 67/33, 85/28
 Nm2156: *pilD*, prepilin leader peptidase 4/16
 Nm2158: conserved hypothetical protein 1/10
 Nm2159: *pilF*, type IV pilus assembly protein 73/27
 Nm2167: hypothetical protein 1/12
 Nm2168: *emrB*, multidrug resistance translocase 33/39, 57/48
 Nm2171: conserved hypothetical inner membrane protein 4/35, 6/20
 Nm2172: conserved hypothetical protein, possible peptidase 6/38
 Nm2174: conserved hypothetical protein 6/41
 Nm2175: *vapA*, possible virulence associated protein 29/25
 Nm2178: conserved hypothetical protein 2/48
 Nm2180: *aroG*, phospho-2-dehydro-3-deoxyheptonate aldolase 78/10
 Nm2183: *opcB*, outer membrane protein 32/30
 Nm2186: hypothetical protein 19/22
 Nm2189: hypothetical inner membrane protein 2/6', 2/10'
 Nm2193: possible TonB-dependent receptor protein 71/23

Nm2200: *dinG*, probable ATP-dependent DNA helicase 83/44
 Nm2204: hypothetical protein 1/23, 3/12
 Nm2212: *trpC*, indole-3-glycerol phosphate synthase 83/13

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Nm1951: unknown 4/6, 37/39
 Nm1953: unknown 80/23
 Nm1957: *fabF2*, 3-oxoacyl-(acyl-carrier-protein) synthase II 11/44, 17/8
Nm1958: *lgtF*, β -1,4-glucosyltransferase 3/15', 23/19', 57/11'', 71/8'', 71/10''
 Nm1960: unknown 2/11
 Nm1961: probable integral membrane ion transporter 10/12
 Nm1969: *mtrD*, probable drug efflux protein 36/36
 Nm1970: *mtrC*, membrane fusion protein 76/30, 92/42
 Nm1973: hypothetical integral membrane protein 2/40, 12/2
 Nm1975: possible integral membrane protein 27/20, 94/9
 Nm1983: *exbD*, biopolymer transport protein 85/3
 Nm1984: *exbB*, biopolymer transport protein 37/33
 Nm1996: *natD'*, possible periplasmic type I secretion system protein, N-terminal region 6/42

 Nm2007: unknown 12/24
 Nm2009: unknown 3/10
 Nm2010: hypothetical protein 5/10, 49/17
 Nm2011: conserved hypothetical protein 94/36, 95/36
 Nm2012: conserved hypothetical protein 43/12
 Nm2016: *speB*, agmatinase 1/46', 42/46'
 Nm2020: possible integral membrane protein 92/18
 Nm2021: possible phospholipase 3/38
 Nm2028: *amiC*, N-acetylmuramoyl-L-alanine amidase 78/47
 Nm2029: unknown 7/21
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 Nm2040: possible integral membrane efflux protein 95/33
 Nm2046: hypothetical integral membrane protein 11/18
 Nm2048: conserved hypothetical protein 41/12, 81/22
 Nm2052: *acnA*, aconitate hydratase 38/25
 Nm2054: *prpC*, citrate synthase 2 8/28, 91/29, 96/30
 Nm2069: probable integral membrane protein 3/4, 31/5
 Nm2076: conserved hypothetical protein 13/2
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 Nm2084: *putA*, bifunctional PutA protein 13/42, 16/10
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 Nm2092: *nadB*, L-aspartate oxidase 2/4, 47/24
 Nm2098: *mapA*, possible maltose phosphorylase 5/34
 Nm2099: *galM*, aldose 1-epimerase (mutarotase) 11/10

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 Nm2120: hypothetical protein within a region of low G+C % 3/23, 78/24
 Nm2122: hypothetical protein within a region of low G+C % 20/13, 29/3
 Nm2123: *frpC'*, possible partial CDS 16/30
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 Nm2129: *aroE*, shikimate dehydrogenase 49/7
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 Nm2146: *tspA*, *Neisseria*-specific antigen protein 9/9
 Nm2151: *ilvE*, probable branched-chain amino acid aminotransferase 41/31, 66/34
 Nm2155: *pilG*, pilus-assembly protein 2/19, 14/45, 25/19, 67/33, 85/28

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**Figure 2A
(cntd)**

Nm2216: possible hydrolase 75/11
 Nm2218: possible tRNA/rRNA methyltransferase 1/15
 Nm2223: probable ABC transporter 16/9
 Nm2225: *xseB*, exodeoxyribonuclease small subunit 42/37

Nm188 or Nm205: *rfaA*, glucose-1-phosphate thymidyltransferase 27/38', 35/36', 35/39', 37/2', 58/8
 Nm293 or Nm609: *pilC2* or *pilC1*, pilus-associated protein 5/42
 Nm525 or Nm527: *lgtB*, lacto-N-neotetraose biosynthesis glycosyl transferase 3/39
 Nm690 or Nm692: unknown 91/33
 Nm788 or Nm1626: *hlyA* or *hlyC*, exotoxin 3/17, 4/36', 7/36', 9/1, 13/41, 18/36, 19/7, 21/17'', 24/17'', 27/28, 65/27, 67/22
 Nm1167 or Nm1999: possible phage protein 12/37, 18/37
 Nm1169 or Nm2001: unknown 78/44
 Nm1196 or Nm1310: unknown 8/44
 Nm1186 or Nm1301: unknown 49/23, 56/37
 Nm1313 or Nm1852: unknown 20/16
 Nm1780 or Nm1781: doubtful ORFs 94/44

NmB65: hypothetical protein 61/44, 77/4
 NmB69: *siaB*, polysialic acid capsule biosynthesis protein 28/22
 NmB70: *synX*, polysialic acid capsule biosynthesis protein 77/19
 NmB91: hypothetical protein 1/4
 NmB98: ABC transporter, ATP-binding protein 7/23, 65/6, 69/1
 NmB223: hypothetical protein 30/6
 NmB372: hypothetical protein 84/20
 NmB493: hemagglutinin/hemolysin-related protein 11/1, 12/1
 NmB648: hypothetical protein 5/40
 NmB653: MafB-related protein 12/21
 NmB896: integrase 16/22, 43/15, 94/14
 NmB1502: hypothetical protein 4/3, 76/31
 NmB1603 tellurite resistance protein 28/10
 NmB1759: conserved hypothetical protein 9/10
 NmB1768: hemagglutinin/hemolysin-related protein 67/27
 NmB1771: hypothetical protein 29/41
 NmB1772: hypothetical protein 16/25
 NmB1829: TonB-dependent receptor 4/32, 47/2
 NmB1830: putative phosphoglycolate phosphatase 4/10
 NmB1854: hypothetical protein 43/48
 NmB1926: *lgtE*, lacto-N-neotetraose biosynthesis glycosyl transferase 79/25
 NmB2132: transferrin-binding protein-related protein 93/5

NmB497 or NmB1779: hemagglutinin/hemolysin-related protein 14/26, 17/21

Nm2156: *pilD*, prepilin leader peptidase 4/16
 Nm2158: conserved hypothetical protein 1/10
 Nm2159: *pilF*, type IV pilus assembly protein 73/27
 Nm2167: hypothetical protein 1/12
 Nm2168: *emrB*, multidrug resistance translocase 33/39, 57/48
 Nm2171: conserved hypothetical inner membrane protein 4/35, 6/20
 Nm2172: conserved hypothetical protein, possible peptidase 6/38
 Nm2174: conserved hypothetical protein 6/41
 Nm2175: *vapA*, possible virulence associated protein 29/25
 Nm2178: conserved hypothetical protein 2/48
 Nm2180: *aroG*, phospho-2-dehydro-3-deoxyheptonate aldolase 78/10
 Nm2183: *opcB*, outer membrane protein 32/30
 Nm2186: hypothetical protein 19/22
 Nm2189: hypothetical inner membrane protein 2/6', 2/10'
 Nm2193: possible TonB-dependent receptor protein 71/23

 Nm2200: *dinG*, probable ATP-dependent DNA helicase 83/44
 Nm2204: hypothetical protein 1/23, 3/12
 Nm2212: *trpC*, indole-3-glycerol phosphate synthase 83/13
 Nm2216: possible hydrolase 75/11
 Nm2218: possible tRNA/rRNA methyltransferase 1/15
 Nm2223: probable ABC transporter 16/9
 Nm2225: *xseB*, exodeoxyribonuclease small subunit 42/37

 Nm188 or Nm205: *rfbA*, glucose-1-phosphate thymidyltransferase 27/38', 35/36', 35/39', 37/2', 58/8
 Nm293 or Nm609: *pilC2* or *pilC1*, pilus-associated protein 5/42
Nm525 or Nm527: *lgtB*, lacto-N-neotetraose biosynthesis glycosyl transferase 3/39
 Nm690 or Nm692: unknown 91/33
 Nm788 or Nm1626: *fpa* or *fpxC*, exotoxin 3/17, 4/36', 7/36', 9/1, 13/41, 18/36, 19/7, 21/17'', 24/17'', 27/28, 65/27, 67/22
 Nm1167 or Nm1999: possible phage protein 12/37, 18/37
 Nm1169 or Nm2001: unknown 78/44
 Nm1196 or Nm1310: unknown 8/44
 Nm1186 or Nm1301: unknown 49/23, 56/37
 Nm1313 or Nm1852: unknown 20/16
 Nm1780 or Nm1781: doubtful ORFs 94/44

NmB65: hypothetical protein 61/44, 77/4
 NmB69: *siaB*, polysialic acid capsule biosynthesis protein 28/22
 NmB70: *synX*, polysialic acid capsule biosynthesis protein 77/19
 NmB91: hypothetical protein 1/4
 NmB98: ABC transporter, ATP-binding protein 7/23, 65/6, 69/1
 NmB223: hypothetical protein 30/6
 NmB372: hypothetical protein 84/20
 NmB493: hemagglutinin/hemolysin-related protein 11/1, 12/1
 NmB648: hypothetical protein 5/40
 NmB653: MafB-related protein 12/21
 NmB896: integrase 16/22, 43/15, 94/14
 NmB1502: hypothetical protein 4/3, 76/31
 NmB1603 tellurite resistance protein 28/10
 NmB1759: conserved hypothetical protein 9/10
 NmB1768: hemagglutinin/hemolysin-related protein 67/27
NmB1771: hypothetical protein 29/41
 NmB1772: hypothetical protein 16/25
 NmB1829: TonB-dependent receptor 4/32, 47/2
 NmB1830: putative phosphoglycolate phosphatase 4/10
 NmB1854: hypothetical protein 43/48
NmB1926: *lgtF*, lacto-N-neotetraose biosynthesis glycosyl transferase 79/25
 NmB2132: transferrin-binding protein-related protein 93/5
 NmB497 or NmB1779: hemagglutinin/hemolysin-related protein 14/26, 17/21

Figure 2B

	703,864 Nm715	# 1,221,368	NmB91	1,415,494	repeats		1,568,211
2,126,264	2,105,217 Nm2158	2,088,655 Nm2140	2,112,160 Nm2167	1,767,971 Nm1820	658,297 Nm670	2,172,491 Nm2218	2,074,248
2,084,953		2,054,730 Nm2101		236,709 Nm251	2,123,512	2,153,822 Nm2204	948,069 Nm982
1,460,109		repeats	886,418 Nm909		repeats	1,460,937 Nm1558	1,238,879 Nm1334
				857,399 Nm884	272,128 Nm287	878,672 Nm905	687,649 Nm696
	1,698,665 Nm1756	666,979 Nm679	64,843 Nm70	?	1,951,943 Nm2016	1,521,873 Nm1617	927,411 Nm962

POOL I

Figure 2B (cntd)

685,934	1,698,113		2,045,802	?	2,136,820	2,068,820	1,176,767
	Nm1755		Nm2092		Nm2189	Nm2113	Nm1249
1,829,713	2,136,820	1,895,085	1,368,594	# 577,460	703,371	1,756,638	385,514
Nm1901	Nm2189	Nm1960		Nm602	Nm714	Nm1812	Nm414
2,127,931	374,049	2,103,202	1,768,357	?		repeats	1,207,685
		Nm2155					
	279,824	1,818,091	1,147,952	repeats	1,869,663	2,027,616	
	Nm293	Nm1892			Nm1937	Nm2078	
	?	?	1,469,783	?	1,810,265	1,020,046	1,910,464
			Nm1565			Nm1062	Nm1973
repeats			# 343,864	910,624	965,796		2,125,540
				Nm941	Nm1001		Nm2178

POOL 2

Figure 2B (cntd)

568,686 Correia	806,502	49,167	2,018,920 Nm2069	1,437,482 Nm1541	2,005,571	503,304 Nm524
?	1,942,983 Nm2009	1,083,831 Nm1136	2,153,985 Nm2204	1,276,911	# 1,893,655 Nm1958	?
?	?	685,663 Nm693	1,336,951		repeats	674,196 Nm688
FtpA/FtpC						
754,958 Correia	62,408	1,568,177	1,641,852 Nm1709		325,607 Nm348	repeats
	repeats		1,343,347 Nm1448	890,346 Nm915	401,037 Nm428	
					?	repeats
repeats		1,237,170 Nm1331	77,675	?	LgtB1/LgtB2 Nm2021	1,584,660 Nm1665
					1,653,607 Nm1722	

POOL 3

Figure 2B (cntd)

	349,670	NmB1502	695,383	343,862	1,887,296	684,371	?
1,350,469	NmB1830		1,065,606	2,088,549	Nm1951	Nm692	2,104,164
Nm1456				Nm2140	Nm1647		Nm2156
419,047	?	709,626	931,104		?	1,865,887	379,058
Nm445		Nm720				Nm1934	Nm409
1,362,832		?	905,094	1,035,280	1,810,015	?	NmB1829
Nm1467			Nm935	Nm1087	Nm1886		
338,703	2,107,269	2,115,910	?	55,614	1,261,610	1,094,698	635,555
Nm365		Nm2171	FrpA/FrpC	Nm60	Nm1363	Nm1145	
1,756,874	2,067,856		1,602,529	1,343,457	15,654		
Nm1812	Nm2113		Nm1679	Nm1448	Correia		

POOL 4

Figure 2B (cntd)

1,016,505	2,039,081		472,245			923,380	948,460
Nm1056			Nm485			Nm955	
?	1,943,994	1,612,586	repeats			595,277	?
	Nm2010					Nm618	Nm968
839,895	2,054,730	1,820,075			# 1,089,503	1,926,443	
Correia	Nm2101						
306,288	?	?	1,405,189	1,089,647	801,597	33,202	# 1,465,366
Nm325			Nm1507		Nm820	Nm39	
	2,051,725	1,354,690	214,973	1,174,994	83,201	1,377,702	NmB648
	Nm2098	Nm1461	Nm225	Nm1248	Nm84	Nm1482	
873,622	?	1,204,530	?	?	384,917	702,612	
Nm904	PIIC1/PIIC2	Nm1276			Nm414	Nm714	

POOL 5

Figure 2B (cntd)

?	1,015,304		1,552,951	786,706	911,076	repeats	826,894
	Nm1054		Nm1642	Nm801	Nm942		Nm845
390,345	734,004	?	487,348	repeats	repeats	590,156	812,450
Nm422	Nm740		Nm506				
	# 1,013,309	483,345	2,115,983		1,324,691	# 1,481,782	repeats
		Nm503	Nm2171			Nm1575	
489,641	1,536,678		976,660	265,362	1,187,524	repeats	# 1,465,368
			Nm1012	Nm279			
1,136,459	1,633,105	965,302	1,277,441		2,228,347	2,054,513	333,694
Nm1195	Nm1702	Nm1001			Nm2172		
2,120,475	1,934,871	463,974		704,647	614,119	860,806	1,149,676
Nm2174	Nm1996	Nm478		Nm715	Nm631	Nm888	Nm1206

POOL 6

Figure 2B (cntd)

876,733		?		1,319,200	618,039		1,205,001
Nm905				Nm1421			
722,895	# 785,373	810,111		913,047	1,428,643	1,158,431	631,905
Nm730	Nm800	Nm827		Nm944	Nm1533		Nm646
686,146	343,971	1,820,075	717,665	# 1,973,097	620,285	NmB98	repeats
Nm694	Nm372		Nm725	Nm2029	Nm636		
554,460	1,170,289	1,038,614	repeats	718,183	997,777	1,370,110	# 1,465,368
Nm580	Nm1243	Nm1090			Nm1037	Nm1475	
947,591		1,034,406	?	138,690	1,190,428	14,916	937,945
Nm982		Nm1086	FtpA/FtpC	Nm155		Nm18	Nm973
	687,915	?	481,434	2,075,630	745,727	1,314,152	
	Nm696		Nm499		Nm753	Nm1415	

POOL 7

Figure 2B (cntd)

644	1,352,235	1,445,893	1,499,525	343,862	2,115,836	150,856	1,369,492
Nm12		Nm1547	Nm1592			Nm165	Nm1475
1,642,041		2,044,450	1,828,682	2,115,219	?	150,856	
Nm1709			Nm1900			Nm165	
	1,369,492	1,820,075	1,245,859	507,967	983,878	491,581	1,407,434
	Nm1475			Correia	Nm1022	Nm512	
	1,652,248	343,971	2,000,303	666,354	303,392	933,246	1,265,402
	Nm1720	Nm372	Nm2054		Nm319		Nm1366
?	1,269,148	?	1,560,853	1,983,878	1,809,404	1,633,105	873,344
	Nm1369		Nm1646	repeats	Nm1886	Nm1702	Nm904
12,174	958,750	1,359,833	?	707,683	repeats	807,717	
Nm15	Nm995	Nm1466	Nm1966 or 1310			Nm826	

POOL 8

Figure 2B (cntd)

?	repeats	repeats		955,198	609,648		441,981
Fipa/Fipc					Nm629		
2,093,221	NmB1759	1,755,247	# 841,843	1,276,911	644,221	1,339,758	1,878,696
Nm2146			Nm865			Nm1445	
18,431		1,117,688	2,084,938	435,022	886,670	611,115	?
Nm22		Nm1164		Nm457	Nm909	Nm631	
874,549		1,585,203	959,423	repeats	2,054,565		
Nm905		Nm1665	Nm995				
	838,871	1,852,051	798,220	55,167	2,054,319		1,861,837
		Nm1920	Nm817	Nm60	Nm2100		Nm1929
	163,763	892,261	2,042,752	# 1,901,617	1,069,137	1,566,007	1,489,574
	Nm182			Nm1966	Nm1118		Nm1584

POOL 9

Figure 2B (cntd)

	503,134	1,562,753	610,203			1,808,086	?
	Nm524	Nm1647	Nm630			Nm1886	
352,213	775,797	?	1,896,645	654,467	420,833	1,415,342	1,028,000
Nm382			Nm1961		Nm445		Nm1074
1,036,914	722,796		1,315,653	682,133	1,425,908	2,001,393	747,045
	Nm730		Nm1417	Nm690	Nm1528		
repeats	?	2,100,166	repeats		2,054,565		2,068,748
							Nm2113
637,874	1,379,195			1,719,627			822,846
Nm650	Nm1483						
	1,307,638	278,168	745,346			383,780	
	Nm1409	Nm292				Nm413	

POOL 10

Figure 2B (cntd)

NmB493	349,670		1,614,134	851,590		232,002	420,833
			Nm1690	Nm873		Nm247	Nm445
# 799,823	2,052,437	1,459,278	1,262,685	1,027,428	2,086,269	1,696,334	232,000
Nm818	Nm2099	Nm1557	Nm1363	Nm1073	Nm2137		Nm247
# 483,902	1,990,827	1,857,005	1,646,465	?	947,390	1,605,638	718,555
Nm503	Nm2046	Nm1925	Nm1715		Nm981		Nm726
1,082,665	747,103	1,354,680	572,705	?	1,395,005	1,292,265	1,277,299
Nm1134		Nm1460	Nm600			Nm1393	Nm1373
639,823		1,478,537		?	1,253,541	?	
Nm654		Nm1574			Nm1356		
1,107,042	2,086,269	repeats	1,892,121	1,123,351			
	Nm2137		Nm1957	Nm1174			

POOL 11

Figure 2B (cntd)

NimB493	1,911,190	repeats	209,739	1,483,767	236,618	786,706
	Nm1973		Nm221	Nm1577	Nm251	Nm801
repeats	# 1,165,235		298,612		1,353,625	
	Nm1234				Nm1356	
236,490	1,132,888	236,618	NmB653		?	1,941,704
Nm251	Nm1186	Nm251				Nm2007
415,186		?	298,306		2,051,828	2071193
Nm441			Nm307		Correia	Nm2118
	878,949	1,767,075	341,230	?	repeats	
	Nm905	Nm1819	Nm368	Nm1167/Nm1999		
		1,808,168		741,849	1,245,699	
		Nm1886		Nm750	Nm1341	2,060,827

POOL 12

Figure 2B (cntd)

	2,025,485			1,301,518	994,646	1,103,757	
	Nm2076			Nm1401	Nm1034	Nm1152	
	2,082,006		1,097,438	repeats	repeats		180,821
	Nm2131						Nm198
			390,462				
			Nm422				
			1,809,978				
			Nm1886				
				# 2,071,060	# 1,679,952	139,199	# 1,465,368
745,160	?			Nm2117	Nm1740	Nm155	
366,813		1,852,051	repeats	92,107		1,380,378	
Nm397		Nm1920				Nm1485	
?	2,032,849	303,532	1,414,499			62,001	
FtpA/C	Nm2084	Nm320	Nm1519				

POOL 13

Figure 2B (contd)

		1,390,528	1,560,805		709,875	1,184,706
		Nm1491	Nm1646		Nm720	Nm1255
1,417,135		1,378,089	-		2,054,792	
		Nm1483			Nm2101	
						1,696,173
						Correia
						Nm1207
567,352	NmB497 or 1779			815,550		
Nm594				Nm832		675,200
						Nm688
745,160		1,697,450	948,460	1,520,153		1,301,518
		Nm1754				Nm1401
	1,083,772		1,290,607	2,102,277	70,533	?
	Nm1136			Nm2155	Nm73	
						417,289

POOL 14

Figure 2B (cntd)

973,938	2,075,448			1,495,207	1,332,096		1,972,429
Nm1008				Nm1590	Nm1438		
214,969	1,698,716	1,084,893	1,858,309	# 541,225	62,406	2,075,433	782,166
Nm225	Nm1756			Nm567			
666,947		1,232,670	175,446	223,973	611,239	77,675	1,099,411
Nm679		Nm1325	Nm193		Nm631		Nm1149
	1,032,157						472,929
	Nm1084						Nm486
	?	1,366,559	1,611,297				704,647
		Nm1473	Nm1687				Nm715
			?			31,414	1,381,289
							Nm1485

POOL 15

Figure 2B (cnt'd)

274,161	674,198			239,262	1,095,984		
Nm289	Nm688			Nm255	Nm1148		
2,176,234	2,033,365		repeats	1,204,534		# 625,143	?
Nm223	Nm2084			Nm1276		Nm639	
# 483,902			219,573	1,870,725	NmB896		
Nm503			Nm233	Nm1938			
NmB1772	?				# 2,074,494	# 928,376	repeats
					Nm2123		
7,561	1,068,213	FrpA/C		1,295,073		957,570	
Nm10				Nm1395		Nm994	
		1,106,063	1,979,533	472,082			
			Nm2038	Nm485			

POOL 16

Figure 2B (cntd)

			178,647 Nm195	1,810,615 Nm1887		1,892,522 Nm1957
						2,038,918
		70,176 Nm73				
			?			
			NmB497 or 1779			
			948,920	?	1,833,197	2,157,77
335,167						

POOL 17

Figure 2B (cntd)

		1,009,610 Nm1048					?
792,595			363,135	1,222,899 Nm1313		178,647 Nm195	753,229 Nm762
		1,059,662 Nm1111	618,007	1,307,751 Nm1409		298,638	
1,413,590 Nm1518	?		1,880,098 Nm1946			1,225,309 Nm1315	1,810,158
346,481 Nm374	2,002,551		FrpA/FrpC	? Nm1167/Nm1999	346,481 Nm374	1,867,553 Nm1934	
repeats			1,095,057 Nm1146		153,926	# 1,859,121	40,553 Nm48

POOL 18

Figure 2B (cntd)

166,036 Nm184	repeats		1,418,510 Nm1523	1,177,109 Nm1250	1,328,654 Nm1435	FtpA/C	796,864 Nm816
	1,476,286		1,039,018 Nm1090	236,490 Nm251	168,270 Nm185		311,848
1,429,874		746,538 Nm753	333,579	# 1,406,958 Nm1508	2,129,971 Nm2186		854,264 Nm879
1,605,658		745,076 Nm752		1,264,321 Nm1365			
639,823 Nm654	1,353,165 Nm1459		555,530 Nm582	1,397,846 Nm1500		1,717,473 Nm1771	
		147,988 Nm162	60,962 Nm65	2,091,395 Nm2145	repeats		1,484,721 Nm1579

POOL 19

Figure 2B (cntd)

1,499,525 Nm1592		repeats	325,573 Nm348			18,989 Nm24	1,633,760
523,612 Nm546				2,073,687 Nm2122	1,654,150	390,345 Nm422	? Nm1313/1852
	931,104	1,870,638 Nm1937					76,633 Nm77
		683,971 Nm692		repeats			
	1,095,984 Nm1148	1,417,135					1,204,632 Nm1276
			16,188 Nm20				

POOL 20

Figure 2B (cntd)

	1,577,038 Nm1660		1,830,389 Nm1901			
	681,430 Nm690		168,270 Nm185			
	1,221,839 Nm1313	repeats				
1,236,888 Nm1331						
		543,611	repeats			
			328,357 Nm353			?

POOL 22

Figure 2B (cntd)

[illegible]

POOL 23

Figure 2B (cntd)

[illegible]

POOL 24

Figure 2B (cntd)

				965,907 Nm1001	175,369 Nm193		
168,597 Nm185				repeats	978,564 Nm1015		1,520,153
			2,102,998 Nm2155			1,260,973 Nm1362	
1,408,644 Nm1509							
							# 1,857,813 Nm1925
				139,199 Nm155			

POOL 25

Figure 2B (cntd)

		1,117,429 Nm1163					
						7,797 Nm10	969,041

POOL 26

Figure 2B (cntd)

	NmB1603								# 1,477,021	
								NmB69		
								745,727 Nm753		
217,341 Nm228								# 1,292,541 Nm1393		
982,378 Nm1020										

POOL 28

Figure 2B (cntd)

		2,073,103 Nm2122			1,729,621 Nm1786		?
?							
2,122,885 Nm2175			785,375 Nm800				977,978 Nm1015
NmB1771	968,313 Nm1003	1,044,730	# 14,356 Nm17				

POOL 29

Figure 2B (cntd)

							NmB223			
# 1,190,685							repeats			
786,864 Nm802						752,537				
2,031,496 Nm2083										

POOL 30

Figure 2B (cntd)

[illegible]

POOL 31

Figure 2B (cntd)

						2,091,407 Nm2145	
						2,128,791 Nm2183	
						829,314 Nm848	
						916,415 Nm948	
						1,866,868 Nm1934	

POOL 32

Figure 2B (cntd)

	911,904 Nm942					2,084,904		
						2,113,660 Nm2168		
							349,670	1,515,641

POOL 33

Figure 2B (cntd)

1,851,986 Nm1920		1,204,052			1,056,116 Nm1108	1,151,839 Nm1206
611,024 Nm631	1,319,531			1,612,668		
	1,413,502 Nm1518	1,315,330 Nm1417				

POOL 34

Figure 2B (cntd)

1,723,027 Nm1778							
	1,754,133 Correia						
2,711 Nm3					735,966 Correia		
					?		
					1,008,897 Nm1048	Nm188 or 205	
						410,874	

POOL 35

Figure 2B (cntd)

				810,726 Nm828	1,819,643 Nm1894	812,142				
					repeats		1,681,423			
					1,906,710 Nm1969	1,397,846 Nm1500				

POOL 36

Figure 2B (cntd)

	?								
	Nm188 or 205								
1,680,042 Nm1740									
					985,021 Nm1022				
1,924,258 Nm1984							1,887,137 Nm1951		

POOL 37

Figure 2B (cntd)

	271,212 Nm285								
								801,367 Correia	
								2,054,741 Nm2101	2,067,769 Nm2113
# 1,996,593 Nm2052							repeats		

POOL 38

Figure 2B (cntd)

[illegible]

POOL 39

Figure 2B (cntd)

				# 1,089,534	1,425,794 Nm1528		
				repeats	1,561,122 Nm1646		
						437,722 Nm457	
1,272,492 Nm1371			1,350,097 Nm1456				
				180,812			

POOL 40

Figure 2B (cntd)

			1,442,807 Nm1545	2,075,312 Nm2124		181,807 Nm198
1,013,296 Nm1052			1,946,913 Nm2012	629,259 Nm643	NmB896	
1,238,616 Nm1334	1,426,582					
						NmB1854

POOL 43

Figure 2B (cntd)

[illegible]

POOL 44

Figure 2B (cntd).

[illegible]

POOL 45

Figure 2B (cntd)

927.175			1,290,609		325,831 Nm349	
				856,389		
1,478,600 Nm1574	846879 Nm868					
	350,939 Nm380	596,375 Nm619		1,076,184 Nm1126	2,090,752 Nm2142	
	342,700 Nm370			682,470 Nm691		

POOL 46

Figure 2B (cntd)

NmB1829		1,866,786 Nm1934		398,034 Nm425	
565,358 Nm592		258,675 Nm274	597,736 Nm619		
	1,139,697 Nm1200				2,045,558 Nm2092
	1,028,178 Nm1074				
		1,870,396 Nm1937	573,776 Nm601	997,525 Nm1037	
	2,481				142,042 Nm157

POOL 47

Figure 2B (cntd)

1,117,429 Nm1163	2,008,688		# 845,850 Nm867	675,145 Nm688	
		repeats			
	815,746 Nm832				

POOL 48

Figure 2B (cntd)

								1,852,520 Nm1920	2,079,897 Nm2129	
								229,743		
1,944,454 Nm2010									?	
								62,096 Nm67		
?						?		812,107		2,123,497
						repeats				

POOL 49

Figure 2B (cntd)

POOL 50

Figure 2B (cntd)

		1,726,253 Nm1783				?		
						746,768 Nm753		
	?					718,075 Nm725		
	repeats							
		156,537 Nm173						?
	?							

POOL 51

Figure 2B (cntd)

785,007		?	2,057,927	# 2,079,961	?	
Nm800		repeats		Nm2130		
1,352,657	825,538		1,139,697			
Nm1459			Nm1200			
		?	1,709,975			
			Nm1765			

POOL 52

Figure 2B (cntd)

?					

POOL 54

Figure 2B (cntd)

[illegible]

POOL 55

Figure 2B (cntd)

	?						
?	?	repeats					
	927,430	Nm962				1,977,980	Nm2036
	825,132	Nm843			?		
					Nm1186/Nm1301		
						1,406,960	Nm1508

POOL 56

Figure 2B (cnfd)

						1,870,396 Nm1937			
	165,931 Nm184	1,893,893 Nm1958					538,192 Nm560		
1,520,208									
14,463 Nm17					?		555,097 Nm582		
								2,113,675 Nm2168	

POOL 57

Figure 2B (cntd)

Figure 2B (cntd)

					# 1,063,168		
						62,406	
	1,291,501	?	590,114				
		repeats					
		1,101,665		2,038,706			
			1,867,847 Nm1935				?

POOL 59

Figure 2B (cntd)

		866,234 Nm892				
	1,878,224 Nm1944					
			43,350 Nm50			
994,969 Nm1035			351,042			
					160,326	

POOL 60

Figure 2B (cntd)

			474,594 Nm489	409,823 Nm434			
				1,633,760		826,623	
			NmB65			1,547,033 Nm1639	

POOL 61

Figure 2B (cntd)

[illegible]

POOL 62

Figure 2B (cntd)

				1,268,930 Nm1369				
				1,435,284 Nm1540	?			
						1,870,199 Nm1937		

POOL 63

Figure 2B (cntd)

				950,279 Nm987	?			
			?					
			repeats					
				14,916 Nm18				

POOL 64

Figure 2B (cntd)

			2,088,727 Nm2140					
	?					1,485,192 Nm1579		
1,165,463								
	2,097,716 Nm2151							

Figure 2B (cntd)

		?			?		
		repeats			FrpA/FrpC		
314,787		NmB1768					± 1,809,345 NmJ886
2,102,378							
Nm2155							

Figure 2B (cntd)

repeats	1,346,136 Nm1450							
		919,190 Nm952					± 1,074,971	
						534,919 Nm559	2,071,324 Nm2118	
623,563 Nm638								
?								

Figure 2B (cntd)

1,451,507						NmB98		
						785,693		
						Nm800		
							659,299	
							Nm672	

POOL 69

POOL 70

[illegible]

Figure 2B (cntd)

	446,234				748,149	1,089,024	1,893,893
	Nm465				Nm755	Nm1140	Nm1958
?	1,893,893		1,207,721				1,286,858
	Nm1958						
	480,137	39,257				2,142,378	
	Nm497	Nm47				Nm2193	
1,245,859					repeats		
		1,868,210				?	
		Nm1936					
		?	repeats				

Figure 2B (cntd)

			1,286,858	637,868 Nm650			
957388 Nm993							164,476 Nm183

POOL 72

Figure 2B (cntd)

				748,143 Nm755	1,142,245		
							2,144,621
	748,143 Nm755						
		2,105,751 Nm2159					
						964,089 Nm999	
		# 1,286,853			1,068,484 Nm1118		

POOL 73

Figure 2B (cntd)

[illegible]

POOL 74

Figure 2B (cntd)

							473,665
		2,171,290 Nm2216					
	418,933 Nm445						
1,716,539			905,180 Nm935			2,091,541 Nm2145	

POOL 75

Figure 2B (cntd)

						264,485	
1,084,893				1,248,598		1,282,003	
Nm1136				Nm1348			
						1,858,309	
					1,908,190	NmB1502	
					Nm1970		
				1,251,524			
				Nm1351			
			263,064			1,654,334	

Figure 2B (cntd)

				NmB65						
				1,499,525 Nm1592	?					
1,149,317 Nm1206		390,879 Nm422			NmB70					

POOL 77

Figure 2B (cntd)

[illegible]

Figure 2B (cntd)

[illegible]

POOL 79

Figure 2B (cntd)

952,888		169,996	1,704,036			
Nm990		Nm186	Nm1761			
		1,235,126			1,808,405	
					Nm1886	
					1,889,562	81,787
					Nm1953	Nm83
		# 669,444	55,614			
			Nm60			

POOL 80

Figure 2B (cntd)

		?	repeats				1,991,435 Nm2048		
						1,096,557 Nm1148	341,653 Nm369		
									1,994,152

POOL 81

Figure 2B (cntd)

					1,487,405		1,027,590 Nm1073		
					2,166,913 Nm2212				
						2,148,926 Nm2200			

POOL 83

Figure 2B (cntd)

?	345,511 Nm374						
1,035,282 Nm1087		NmB372					

POOL 84

Figure 2B (cntd)

Figure 2B (cntd)

						673,742 Nm688			
					1,612,674				1,316,522 Nm1418
									1,333,468 Nm1440
					983,518				

POOL 87

POOL 88

[illegible]

POOL 89

[illegible]

Figure 2B (cntd)

			1,022,411			943,634	
						Nm977	
	1,475,430 Nm1571	945,311 Nm979		?			
		1,404,807 Nm1507	?	753,485 Nm762	1,695,410 Nm1751		
1,901,182	739,862 Nm747		509,985 Nm531				328,357 Nm353
		1,248,814	2,056,120 Nm2101	625,404 Nm639		1,328,414 Nm1435	

Figure 2B (cntd)

	571,814 Nm599	1,321,363 Nm1425					
1,613,820 Nm1689						1,443,339	
				2,000,734 Nm2054			
?							?
Nm690 or 692							
595,277 Nm618		2,109,838				289,906	

Figure 2B (cntd)

	780,313		976,649	1,369,405			
	Nm796		Nm1012	Nm1475			
2,085,389	148,703	243,185	1,369,405	1,558,864		734,251	
Nm2136		Nm259	Nm1475	Nm1645		Nm741	
	1,956,664			1,767,251	1,269,498	1,092,318	
	Nm2020			Nm1819	Correia	Nm1143	
# 206,285		1,183,770	1,239,706	# 1,086,735		repeats	1,290,609
Nm220		Nm1255		Nm1139			
		142,196	144,763				
			Nm160				
590,283	1,907,294	721,054	# 1,369,654	595,277			
Nm613	Nm1970	Nm729	Nm1475	Nm618			

POOL 92

Figure 2B (cntd)

?	repeats	62,404	?	NmB2132			24,221 Nm29
?	1,225,330	994,900	1,763,435	33,002	1,287,708	1,658,462	repeats
	Nm1315	Nm1035	Nm1816		Nm1385		
491,378	1,103,537	170,104					
	Nm1152	Nm186					
788206		?		1,331,057	422,265	866,358	412,800
Nm804							Nm436
1,860,457	618,039		?	?	217,751		849,737
Nm1928					Nm229		
	1,648,062	239,013	979,379	625,475	1,720,495	178,214	?
		Nm255	Nm1016	Nm639	Nm1775	Nm195	

Figure 2B (cntd)

	966,344 Nm1001						1,068,488 Nm1118
1,915,903 Nm1975					NmB896	1,184,157 Nm1255	
314,780	967,253 Nm1002	1,873,509 Nm1940				265,540	1,257,099
	1,080,375	1,664,669 Nm1731	279,302 Nm293			1,101,935	2,179,156
		1,222,561 Nm1313	1,945,709 Nm2011	# 1,211,124 Nm1285	236,897 Nm251	# 575,138 Nm602	?
?			1,725,097 Nm1780 or 1781		?	1,859,281	1,413,563 Nm1518

Figure 2B (cntd)

	1,200,238		2,042,752	827,895	1,103,507		1,280,372
	Nm1272			Nm847	Nm1152		Nm1375
898,986	1,867,841	?		392,893	291,442		=319,551
Nm928	Nm1935				Nm298		
489,643						151,594	
						Nm165	
# 1,357,825	?						1,219,964
Nm1465							Nm1307
1,981,237			1,945,709	32,210		863,804	
Nm2040			Nm2011	Nm37		Nm890	
				745,456	?	265,348	1,559,590
				Nm753		Nm279	Nm1646

POOL 95

Figure 2B (cntd)

1,116,609	1,085,727	654,474		1,729,378		?	1,056,050
Nm1162	Nm1138			Nm1786			Nm1107
	1,487,870	596,933		1,509,295		1,728,474	927,970
		Nm619		Nm1603		Nm1785	Nm962
	?			2,038,850		572,193	1,654,720
						475,258	
						Nm490	Nm599
1,890,936						2,000,669	800,429
						Nm2054	Nm819
	1,713,480	351,040	?	?		1,917,966	744,040
	Nm1767						Nm752
			repeats			672,238	2,086,387
						Nm687	Nm2137
							1,559,479

Figure 3

ORF No. <i>N.meningitidis</i> B / <i>N.meningitidis</i> A	Identified genes	Associated mutants	Phenotype observed
NmB71/Nm198	<i>ctrA</i> , capsule export outer membrane protein	43/8	capsule +/-
NmB72/Nm197	<i>ctrB</i> , capsule export inner-membrane protein	40/45	capsule +/-
NmB73/Nm196	<i>ctrC</i> , capsule export inner-membrane protein	85/40	capsule +/-
NmB74/Nm195	<i>ctrD</i> , capsule export ATP-binding protein	93/47, 18/15	capsule +/-
NmB70	<i>siaA</i> , sialic acid biosynthesis protein	77/19	capsule -
NmB69	<i>siaB</i> , sialic acid biosynthesis protein	28/22	capsule +/-
	intergenic region <i>siaA-ctrA</i>	3/16	capsule +
NmB82/Nm186	<i>lipA</i> , capsule phospholipid modification protein	58/48, 41/29	capsule -
NmB83/Nm185	<i>lipB</i> , capsule phospholipid modification protein	19/14, 22/14, 80/24, 86/2, 29/41	capsule -
Nm1929/Nm524	<i>lgtA</i> , lacto-N-neotetraose biosynthesis glycosyl transferase	56/17, 21/21	truncated lipooligosaccharide
NmB1926	<i>lgtE</i> , lacto-N-neotetraose biosynthesis glycosyl transferase	3/39	truncated lipooligosaccharide
NmB1704/Nm198 ₅	<i>lgtF</i> , β -1, 4- glucosyl transferase	71/8, 3/15, 23/19	truncated lipooligosaccharide
NmB828/Nm1037	<i>rfaD</i> , ADP-L-glycero-D-mannoheptose epimerase	47/39, 7/30	truncated lipooligosaccharide
NmB825/Nm1034	<i>rfaE</i> , ADP-heptose synthetase	13/6	truncated lipooligosaccharide
NmB790/Nm1001	<i>pgm</i> , phosphoglucomutase	25/5, 94/2, 92/48	truncated lipooligosaccharide
NmB638/Nm848	<i>galU</i> , UTP-glucose-1-phosphate uridylyltransferase	32/37	truncated lipooligosaccharide
Nm2076/Nm356	<i>aut</i> , possible cytidylyltransferase	55/48	truncated lipooligosaccharide
NmB065	hypothetical protein	61/44, 77/4	capsule +/-
NmB352/Nm1035	sugar isomerase	33/7	none

Figure 4A

□ *ctrA*, capsule export outer membrane protein (NmB71): mutant 43/8

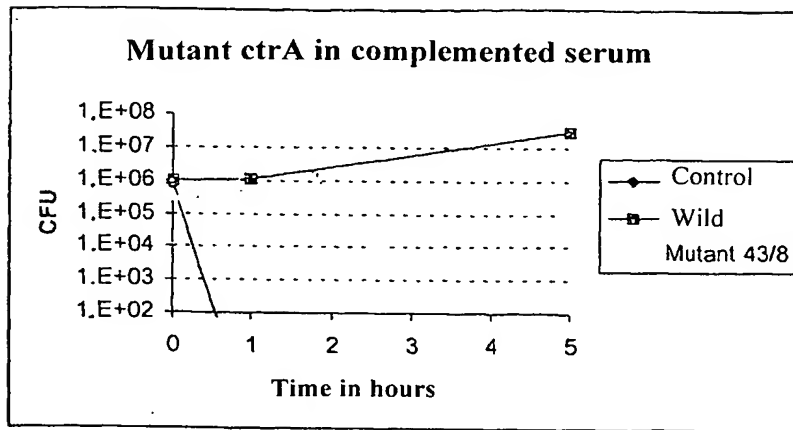
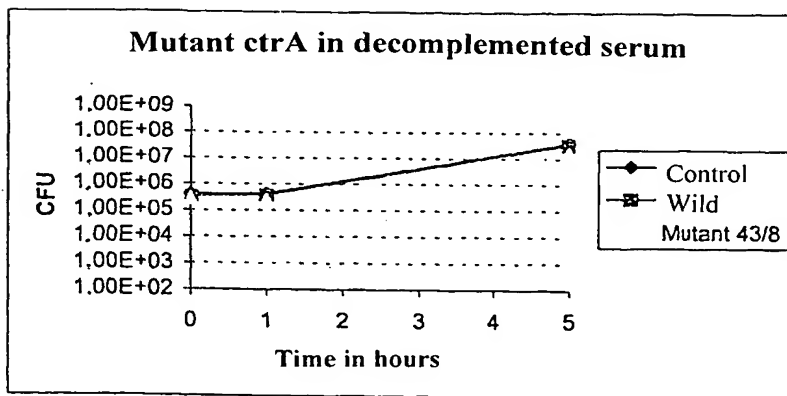
Figure 4B

Figure 5A

- just ahead *ctrB*, capsule export inner-membrane protein (NmB72): mutant 40/45

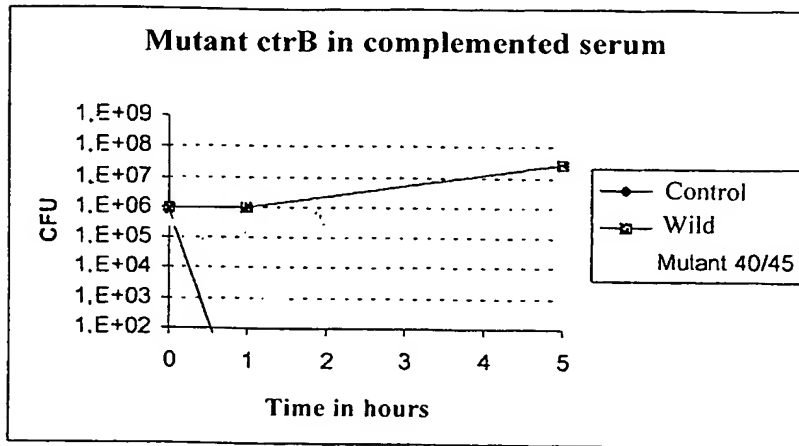
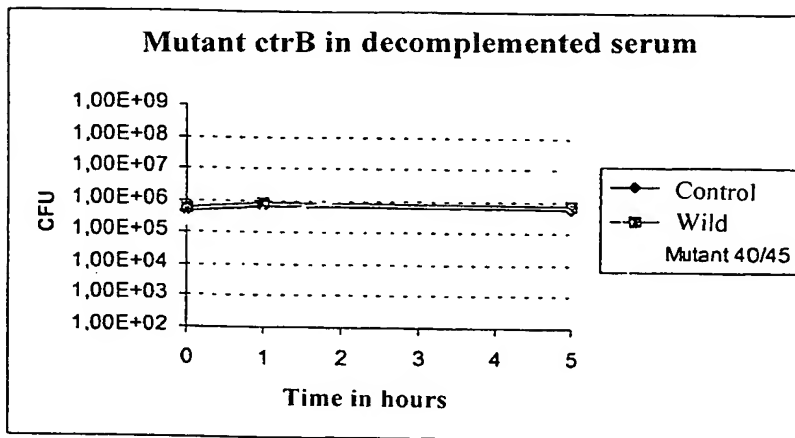
Figure 5B

Figure 6A

□ *ctrC*, capsule export inner-membrane protein (NmB73): mutant 85/40

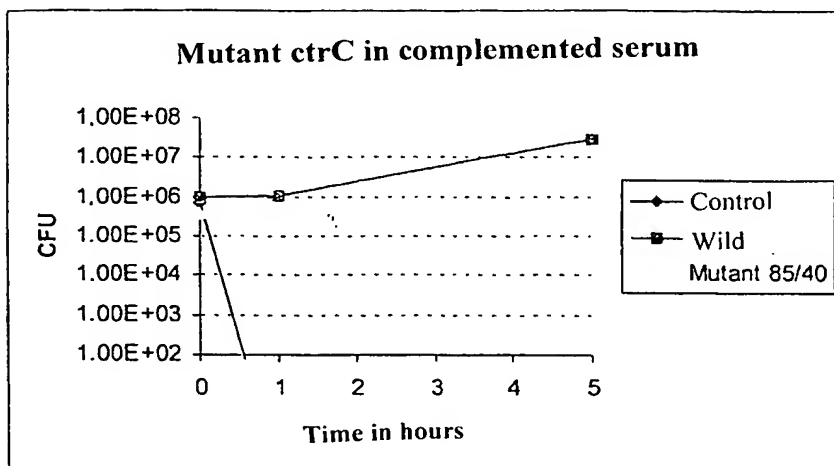
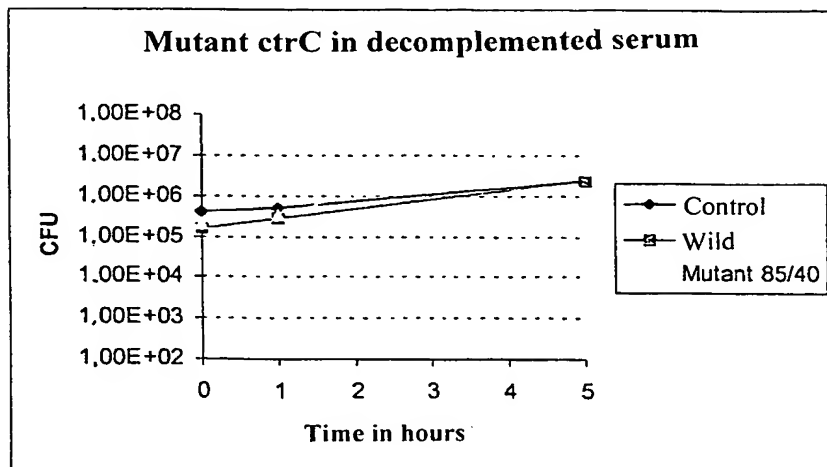
**Figure 6B**

Figure 7A

□ *ctrD*, capsule export ATP-binding protein (NmB74) : mutant 93/47

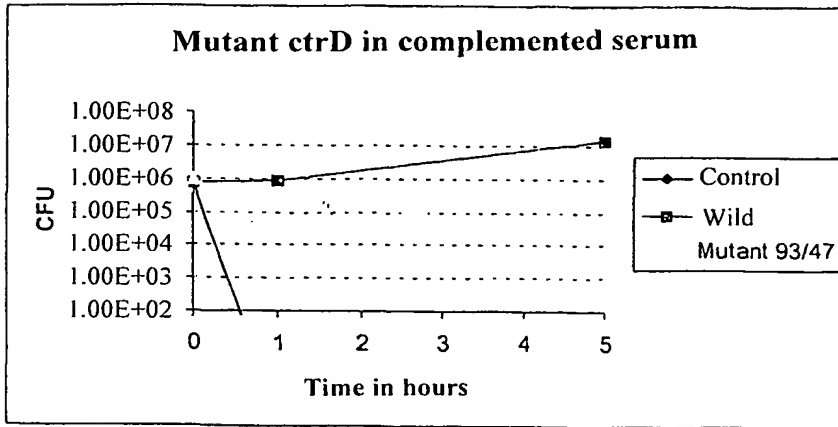
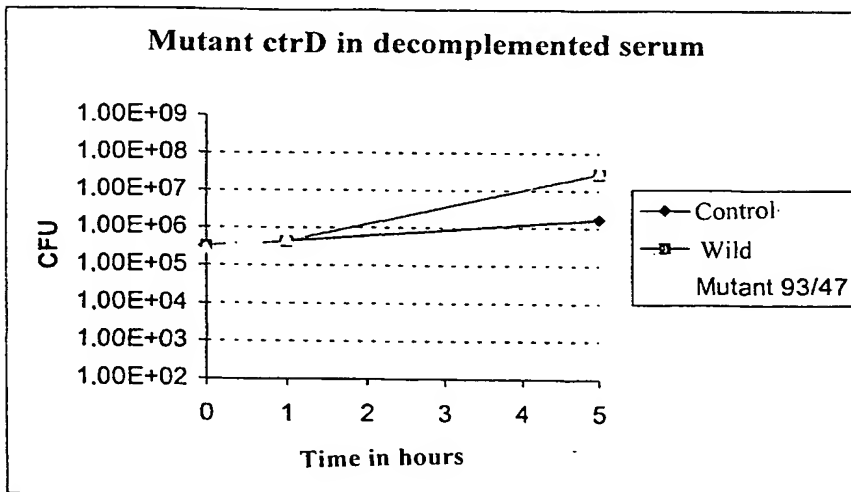
**Figure 7B**

Figure 8A

□ *siaA*, sialic acid biosynthesis protein (NmB70) : mutant 77/19

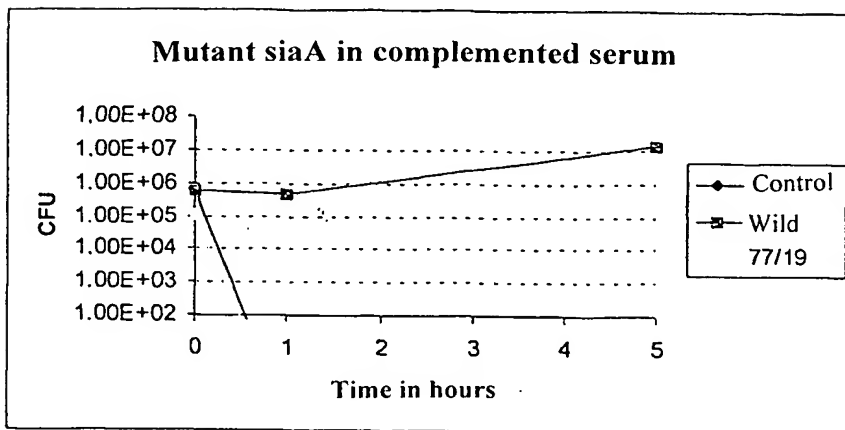
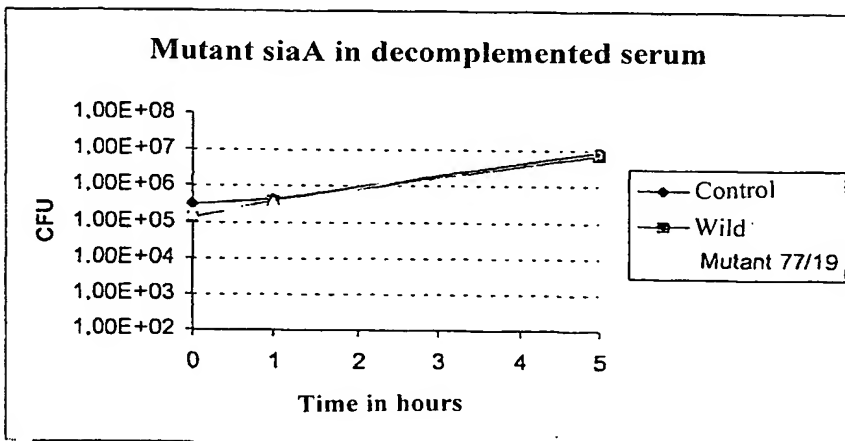
**Figure 8B**

Figure 9A

□ *siaB*, sialic acid biosynthesis protein (NmB69) : mutant 28/22

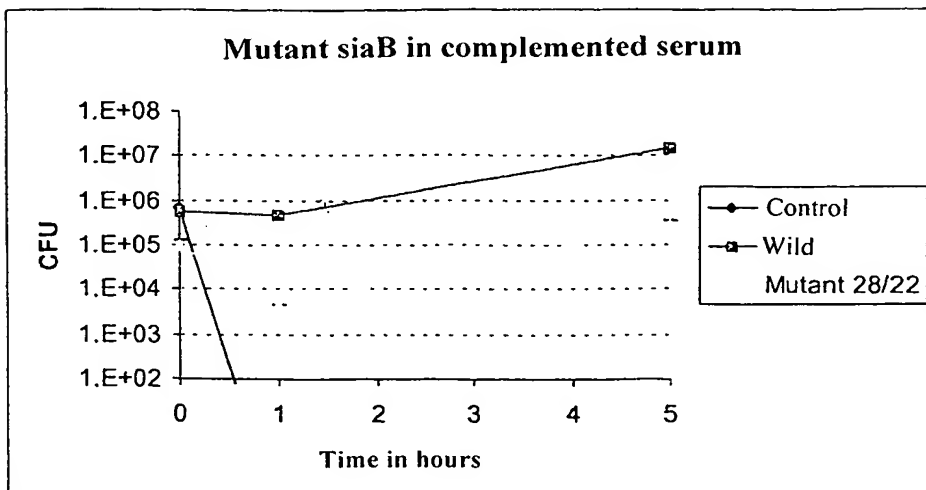
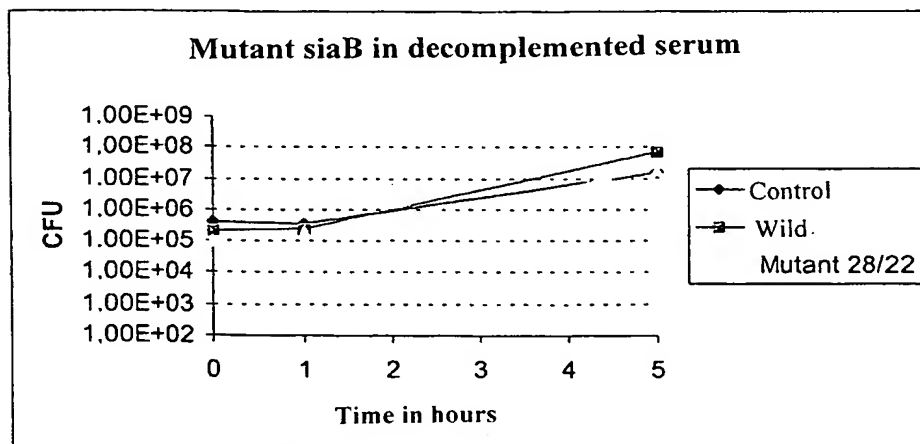
**Figure 9B**

Figure 10A

□ *siaA-ctrA*, intergenic region: mutant 3/16

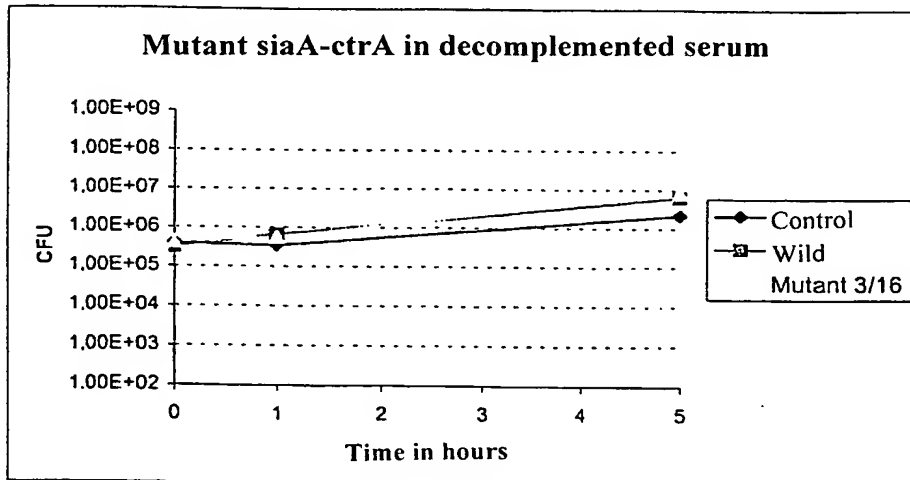
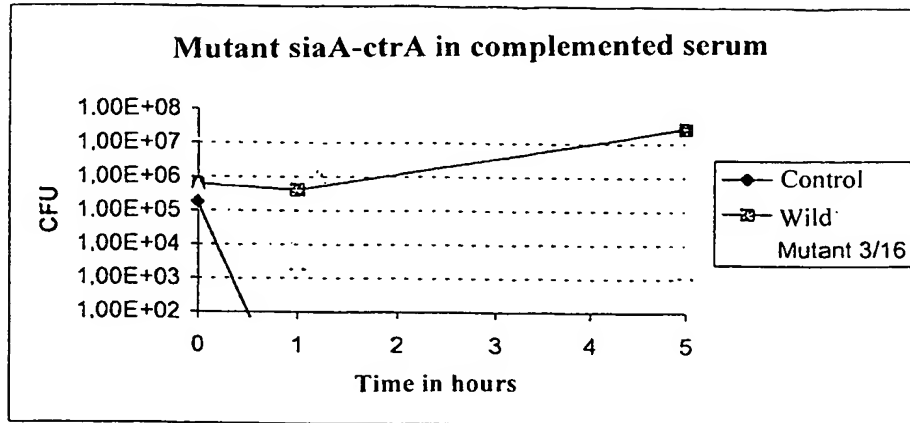
**Figure 10B**

Figure 11A

□ *lipA*, capsule phospholipid modification protein (NmB82) : mutant 58/48

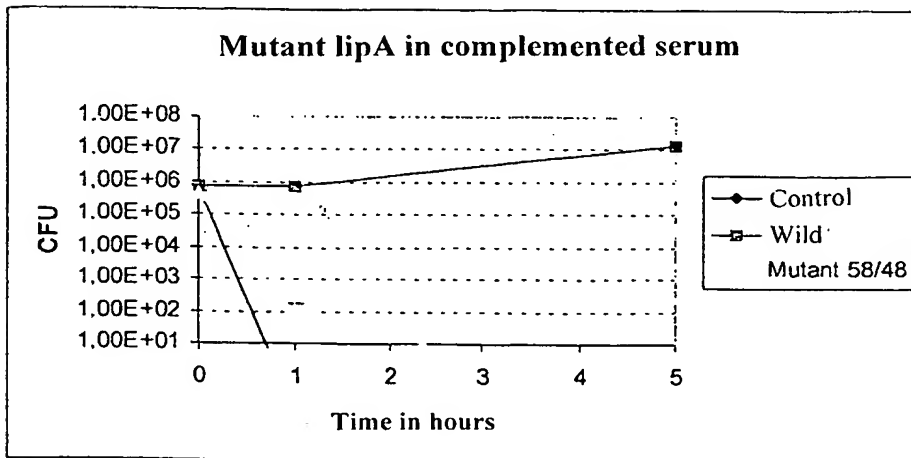
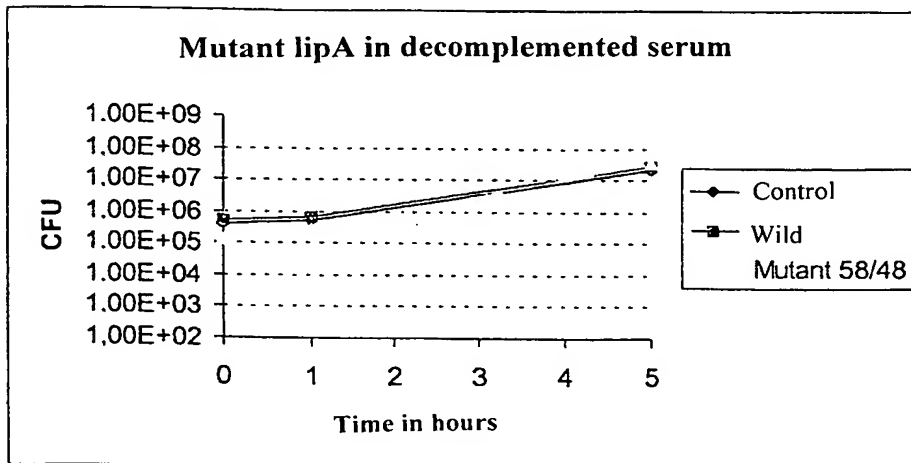
**Figure 11B**

Figure 12A

□ *lipB*, capsule phospholipid modification protein (NmB83): mutant 19/14

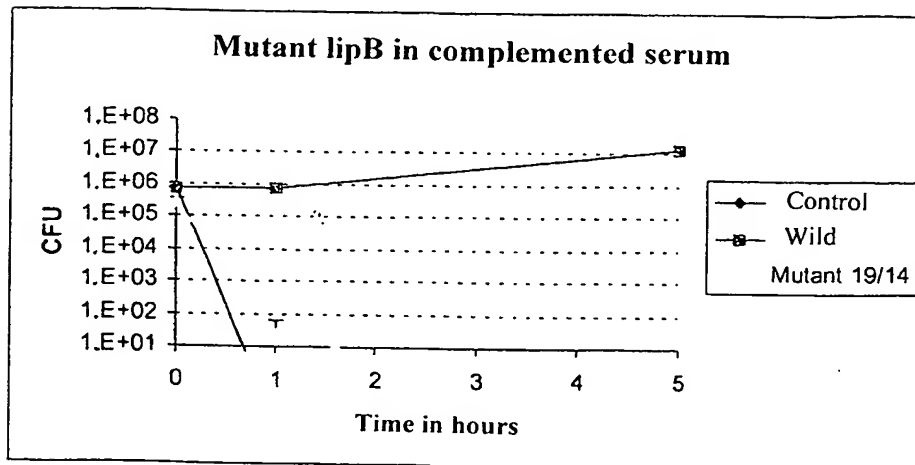
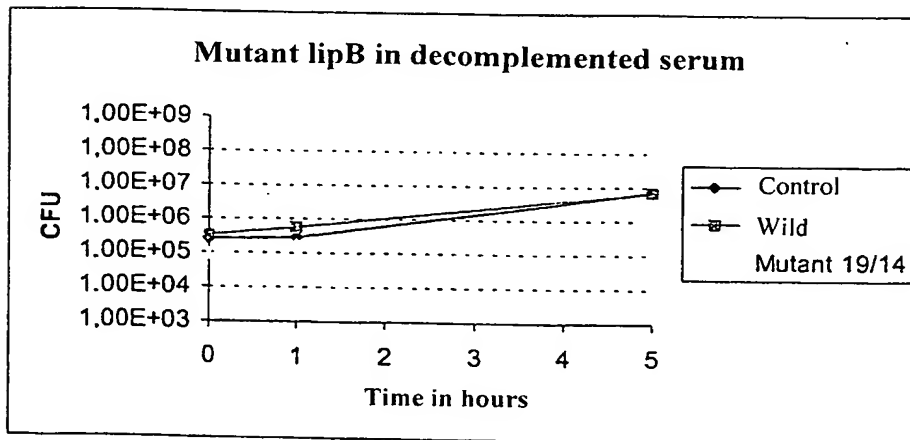
**Figure 12B**

Figure 13A

- *IgtA*, lacto-N-neotetraose biosynthesis glycosyl transferase (NmB1929): mutant 56/17

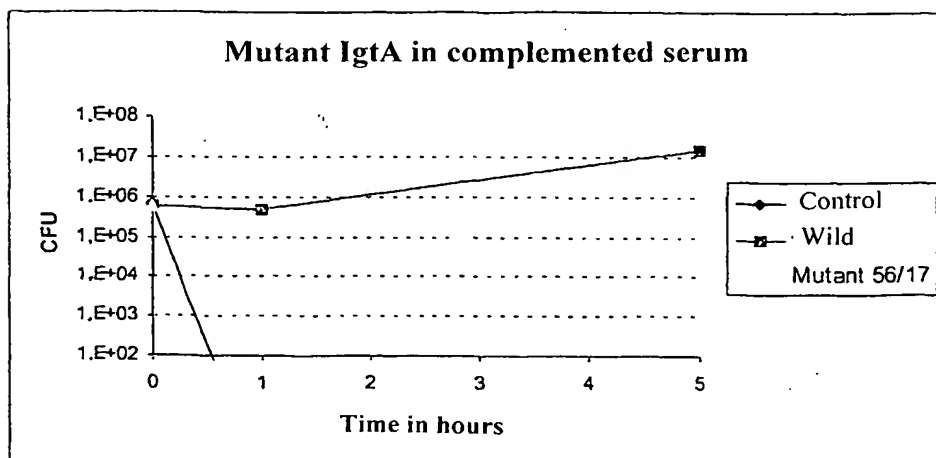
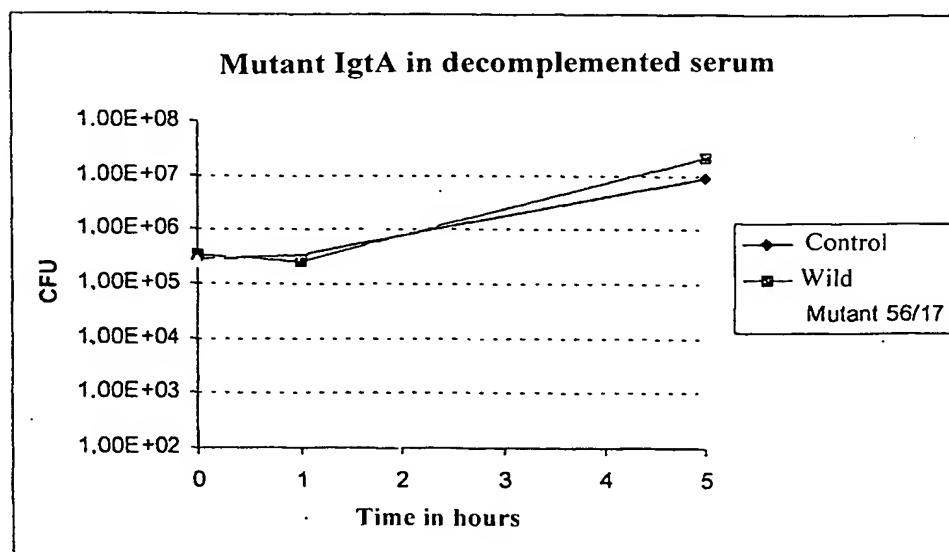
**Figure 13B**

Figure 14A

- *IgtE*, lacto-N-neotetraose biosynthesis glycosyl transferase (NmB1926): mutant 3/39

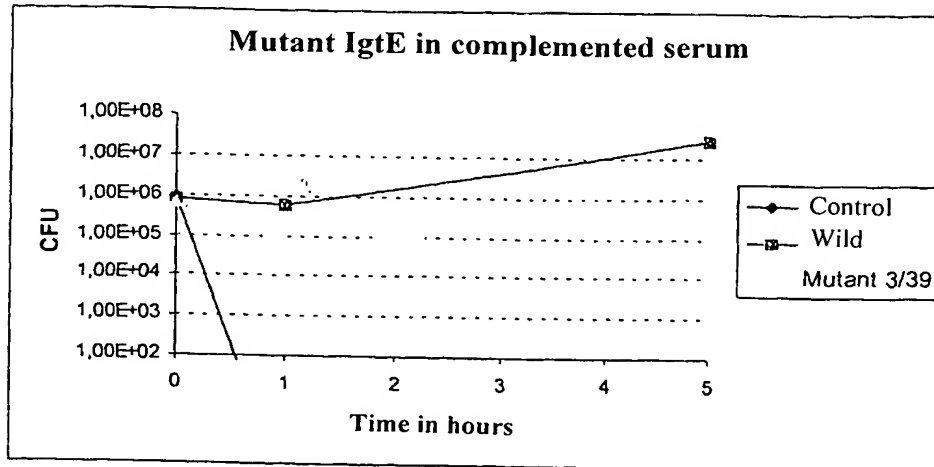
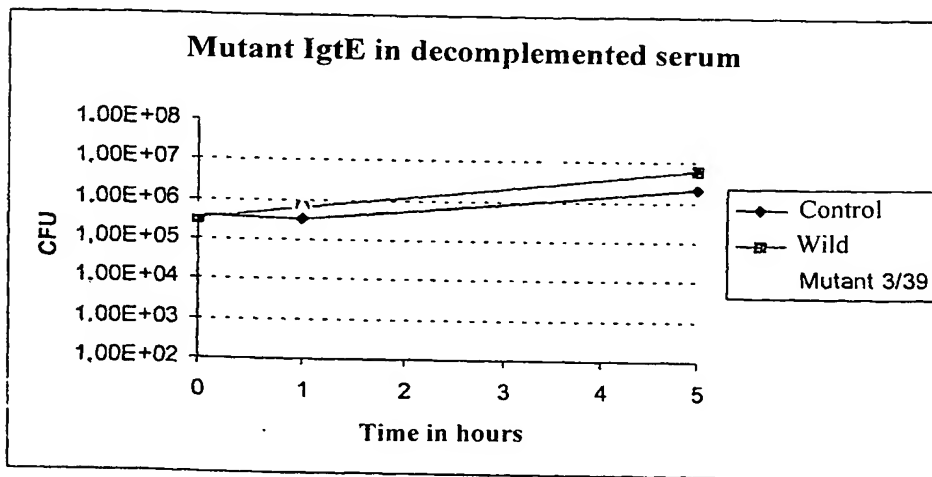
**Figure 14B**

Figure 15A

□ *IgtF*, -1, 4- glucosyl transferase (NmB1704): mutant 71/8

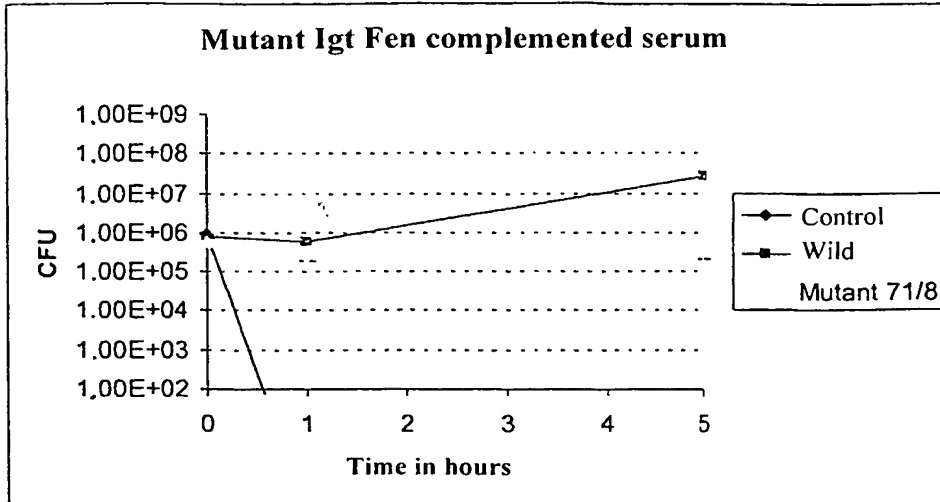
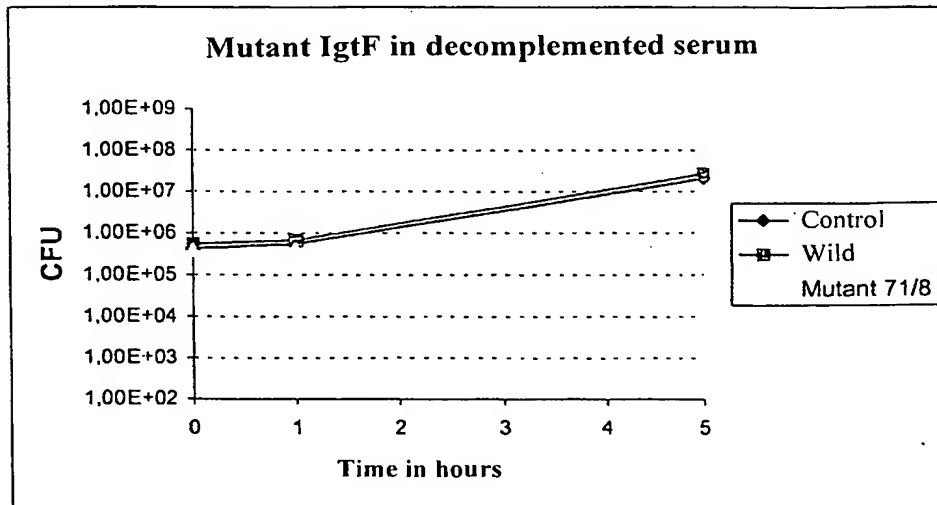
Figure 15B

Figure 16A

□ *rfaD*, ADP-L-glycero-D-mannoheptose epimerase (NmB828): mutant 47/39

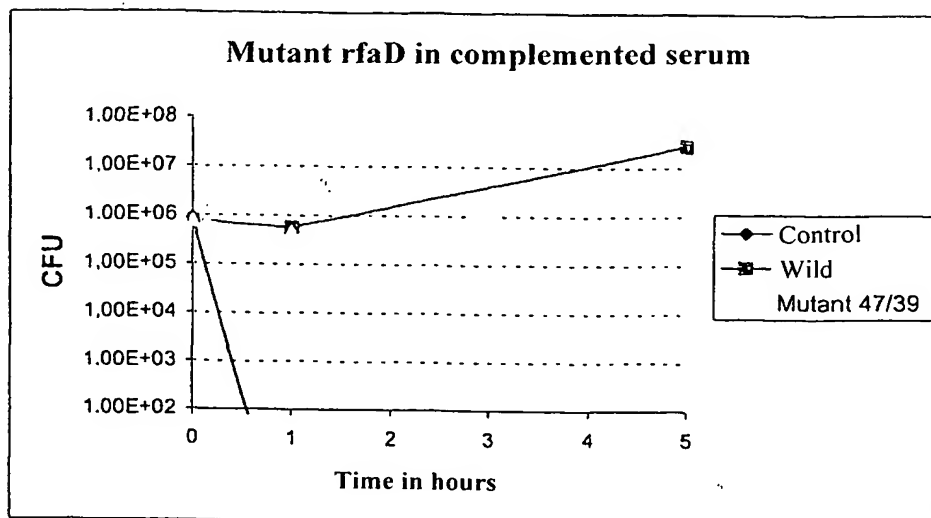
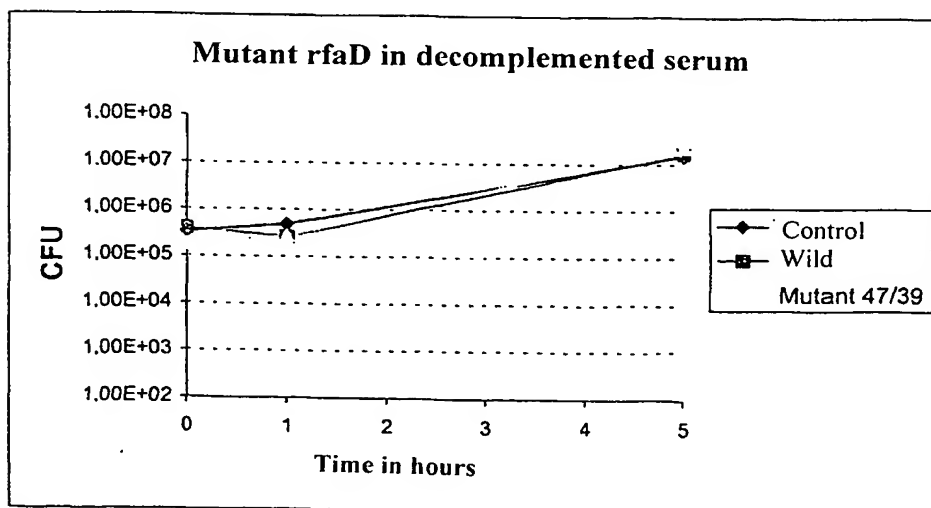
**Figure 16B**

Figure 17A

□ *rfaE*, ADP-heptose synthetase (NmB825) : mutant 13/6

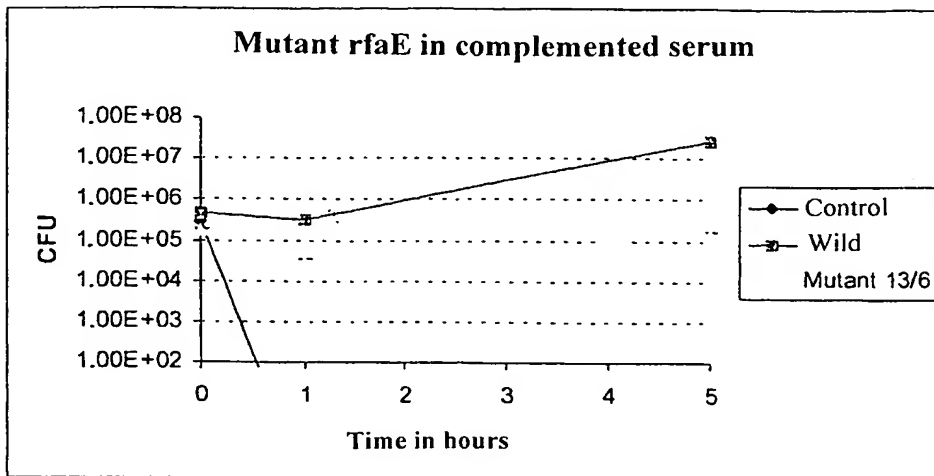
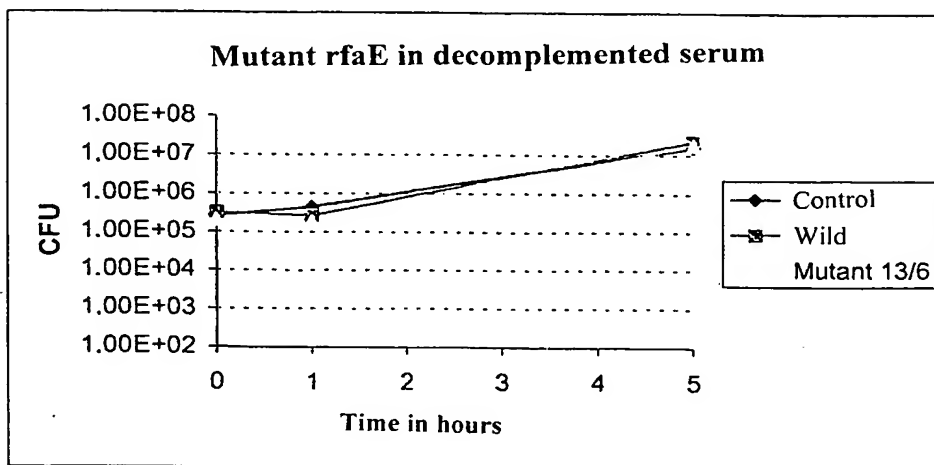
Figure 17B

Figure 18A

□ *pgm*, phosphoglucomutase (NmB790): mutant 25/5

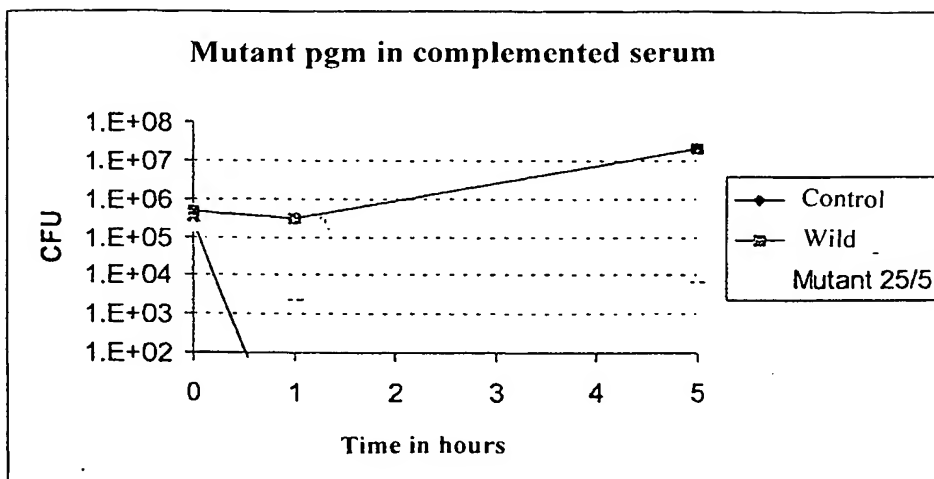
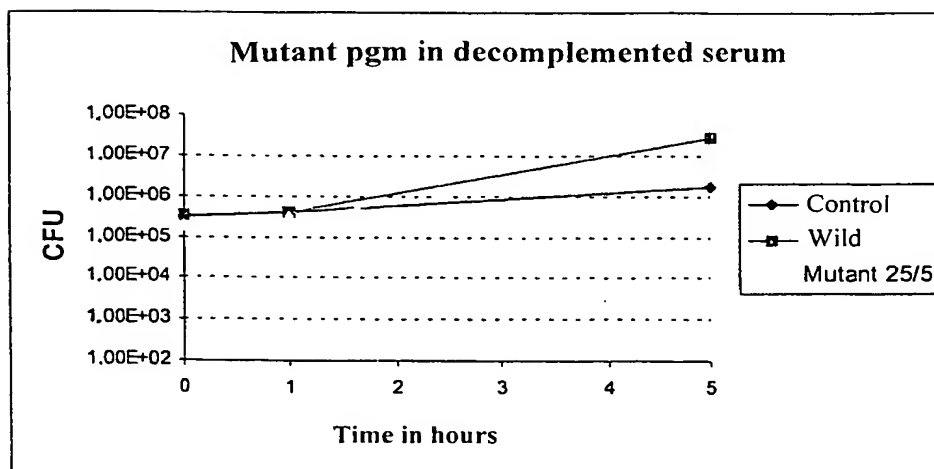
**Figure 18B**

Figure 19A

□ *galU*, UTP-glucose-1-phosphate uridylyltransferase (NmB638): mutant 32/37

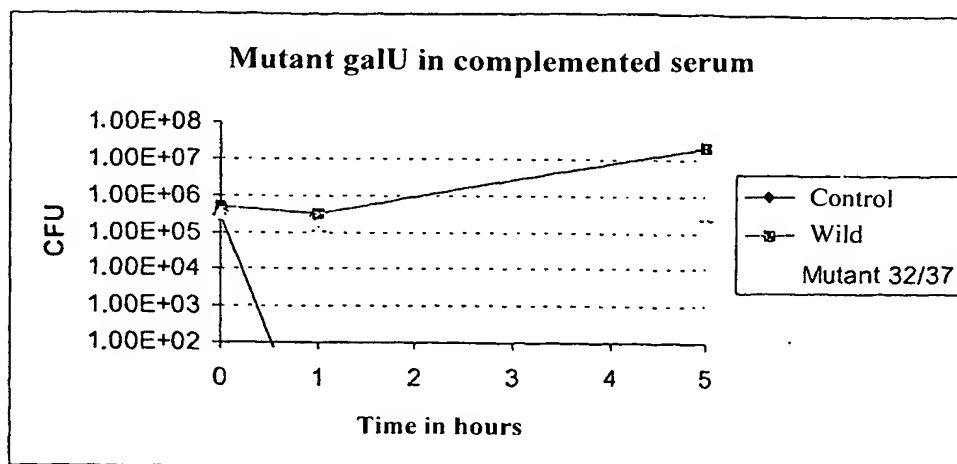
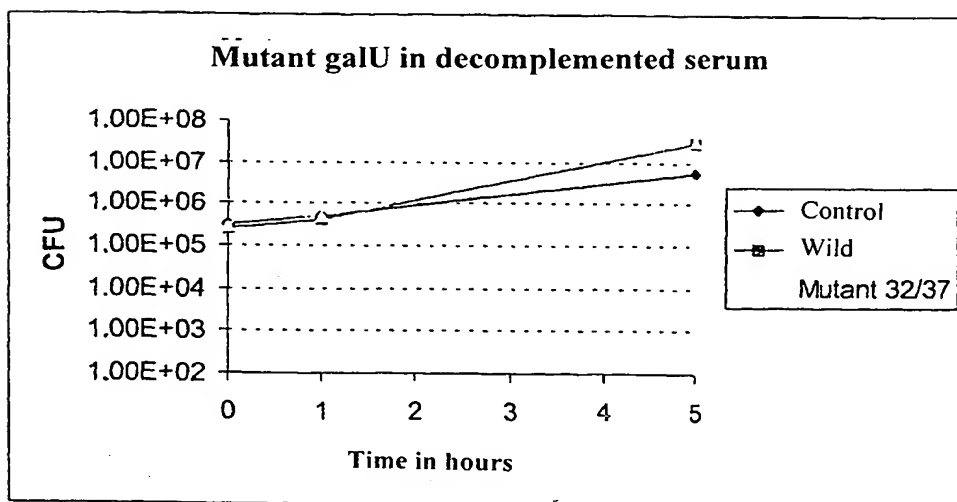
**Figure 19B**

Figure 20A

□ *aut*, possible cytidylyltransferase (NmB2076) : mutant 55/48

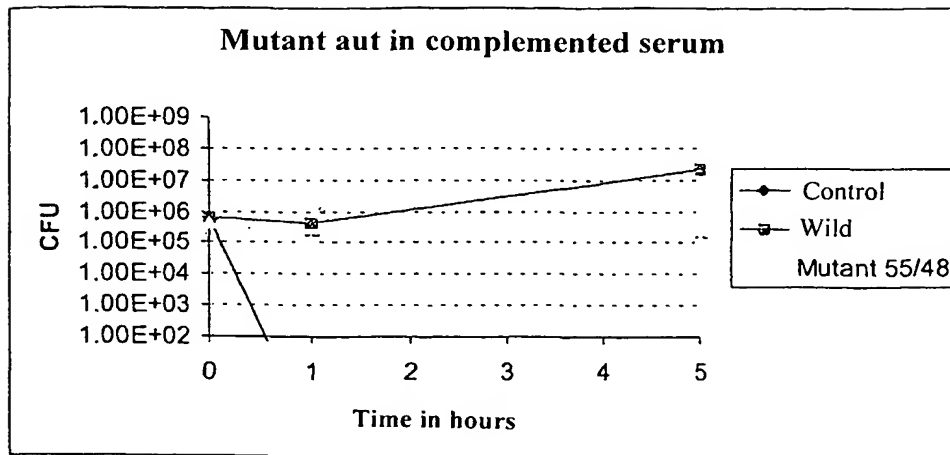
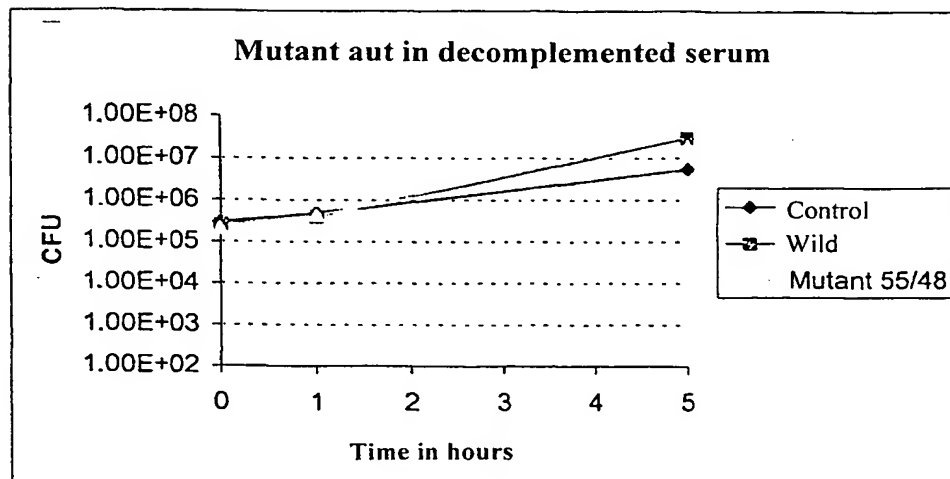
**Figure 20B**

Figure 21A

□ hypothetical protein (NmB065): mutant 61/44

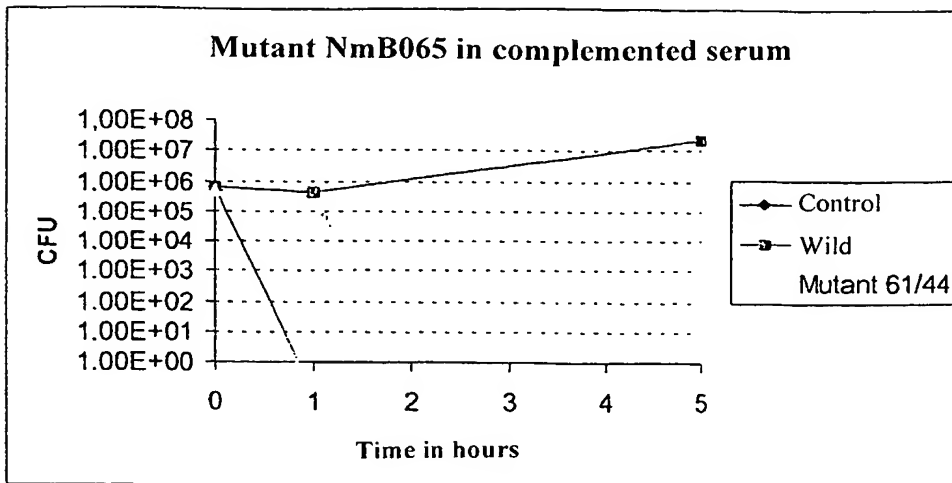
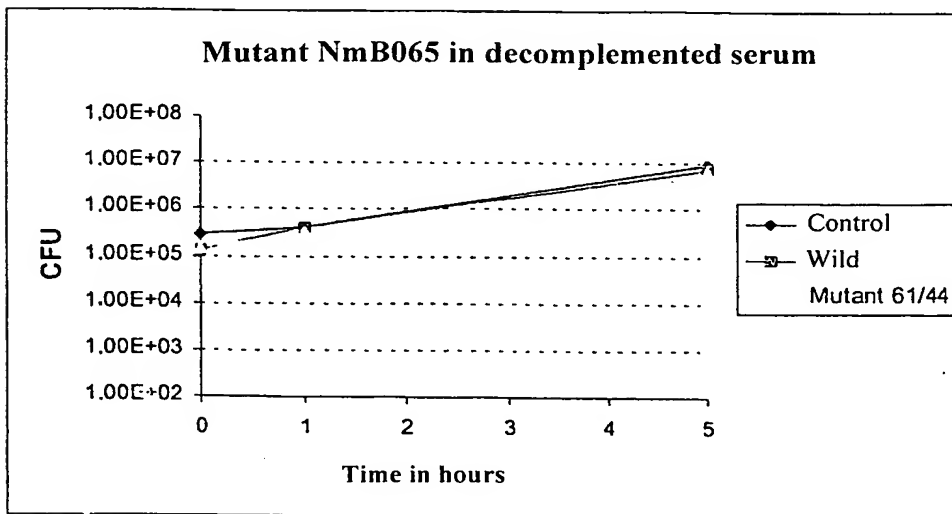
**Figure 21B**

Figure 22A

□ just ahead sugar isomerase (NmB352): mutant 33/7

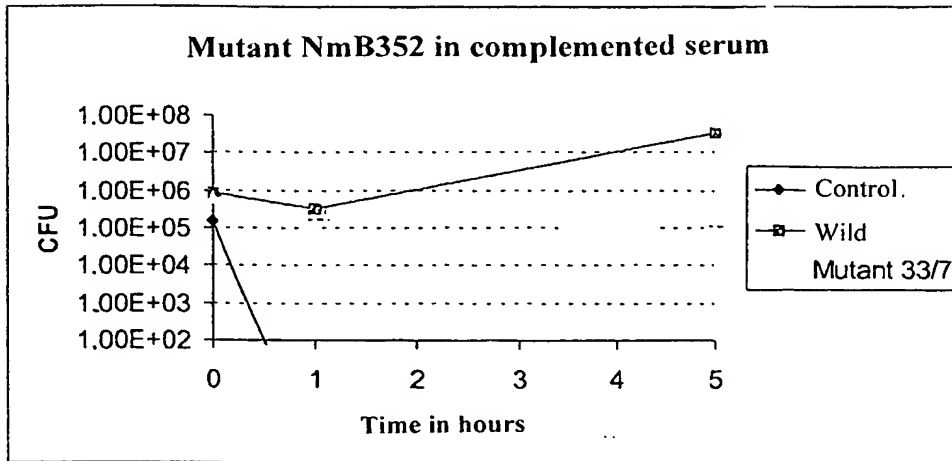
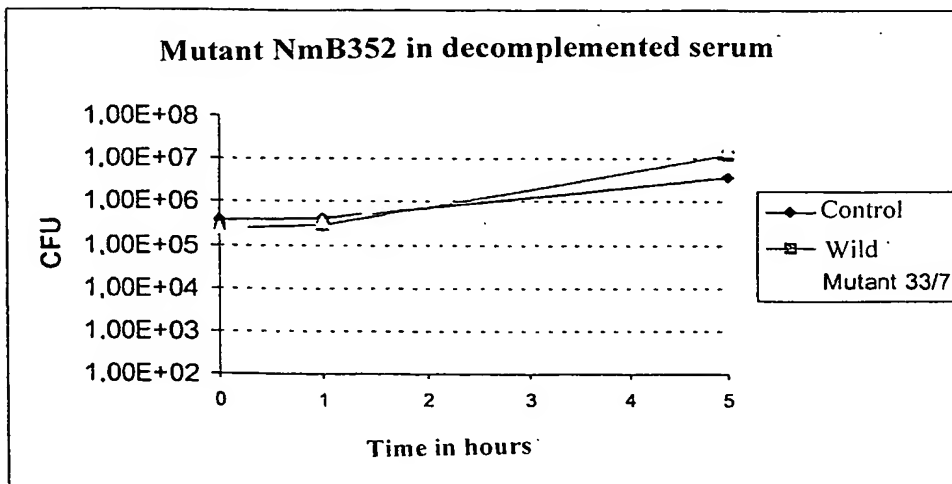
**Figure 22B**

Figure 23A

□ unknown gene: mutant 63/19

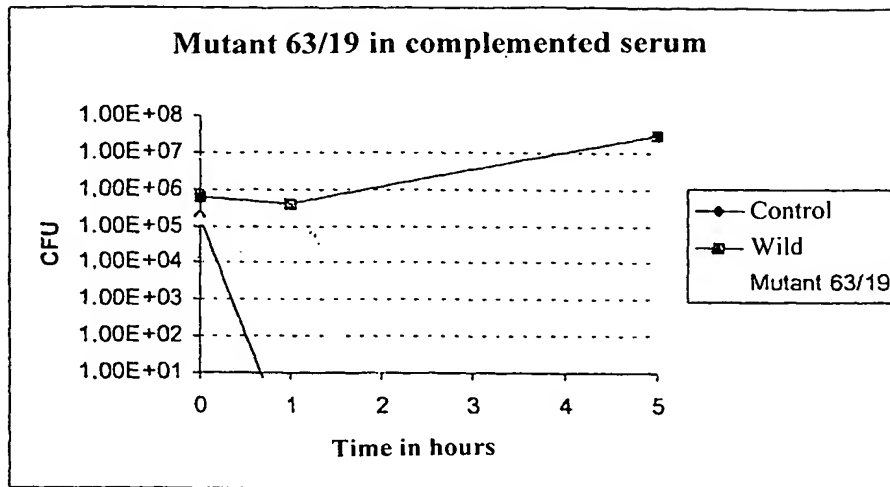


Figure 23B

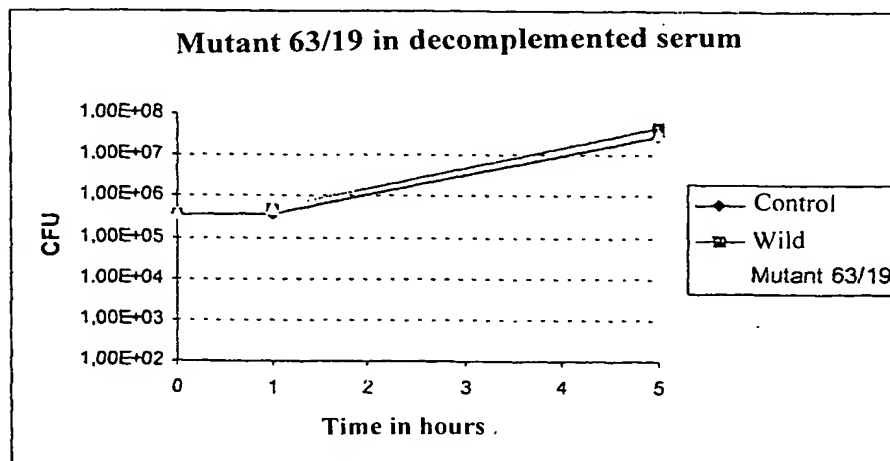
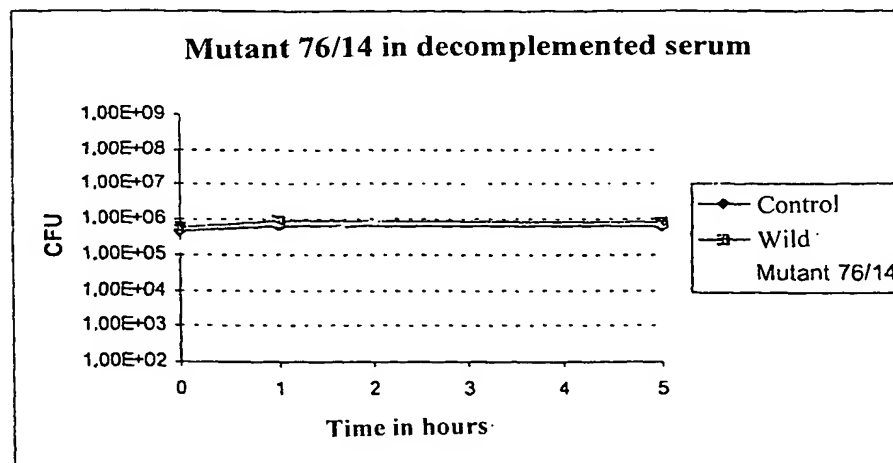
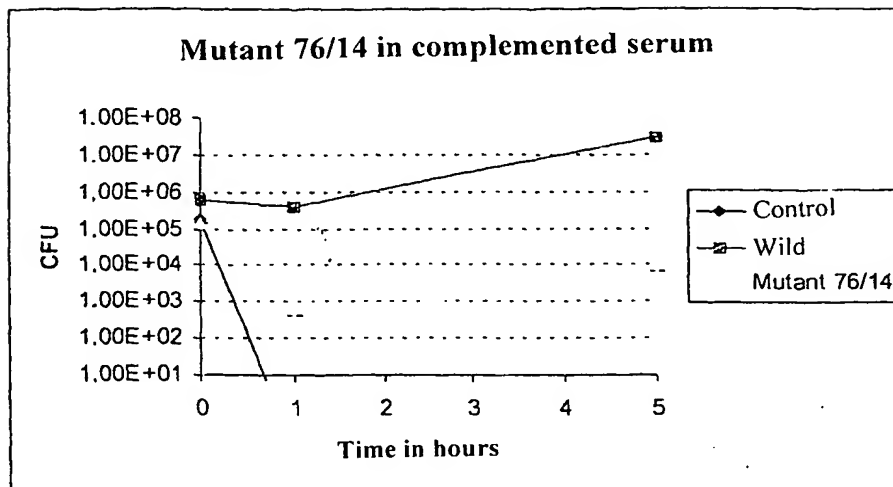


Figure 24A

□ unknown gene: mutant 76/14

**Figure 24B**

received 18/09/02

D

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